

Supplemental Data**Global Mapping of c-Myc Binding Sites and Target Gene Networks in Human B Cells**

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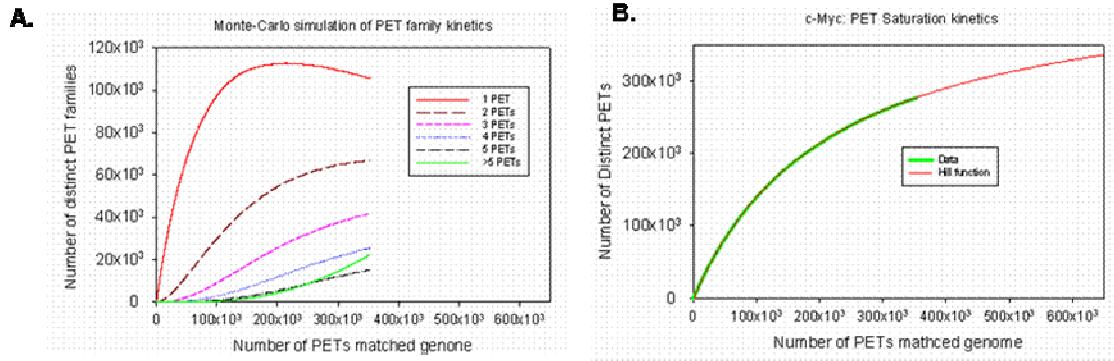
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I. Supplemental Analysis

I-1 Myc ChIP-PET library saturation kinetics and detection sensitivity

Myc ChIP DNA was cloned as a PET library for sequencing analysis. To estimate the maximum number of unique ChIP DNA fragments captured in the original cloned ChIP library, we performed saturation analysis. From a total of 691,966 PET sequences mapped specifically to hg17 genome, 273,566 distinct PETs were defined, and the distribution of these 273,566 sequences by their abundance follows an exponential distribution function, where 38% (105,520) of the 273,566 sequences were represented by a single copies and only 0.93% (2,568) of 273,566 sequences were represented by 10-24 copies. The mean value is 2.55 PET sequences per unique sequence. We assumed that as the number of PET sequences increases, the diversity of the PET sequences must increase and discovery rate of distinct PET fragments decreases. Due to a finite number of the distinct PET clusters associated with a finite number of Myc binding sites; the number of distinct PET singletons will gradually decrease when the library size increases. The total number of PET fragments identified should plateau when diversity in the library approaches saturation level. To generate the saturation curve of the number of distinct PETs as a function of the number of slPETs (random sampled PETs), we first, sequentially selected (without replacement) a series of random subset of size 100 slPETs from our 691,966 PET sequences, added such subset to previously selected slPETs sample and then counted the number of distinct PETs in the increasing samples of slPETs. This procedure assumes that each new PET sequence has occurred in the library randomly and independently. Figure I-1A provides detail kinetics for families of distinct PETs, which are represented by 1, 2, 3, 4, 5 and more than 5 copies PETs per each distinct PET. This figure shows that the number of singleton PETs monotonously increases and dropped down, while the sizes other families (size 2, 3,...) closely approach to their maximum levels.



Supplemental Figure I-1-1. Kinetics of the distinct PET redundancies.

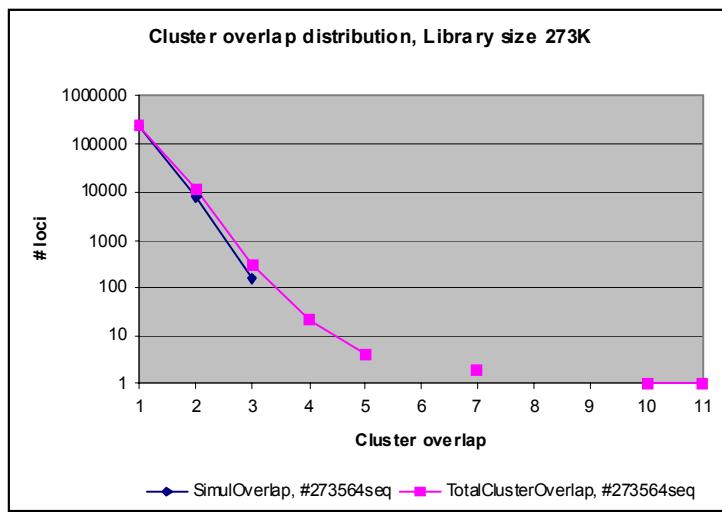
(A). Distributions of PET redundancy were represented by one, 2, 3, 4, 5 and more than 5 copies of PETs per distinct PET. **(B).** Hill-like empirical function curve (green) for estimating the total distinct PETs coverage. Empirical data of PET sequences (green) fitted tightly with the Hill function theoretical curve (red).

The green line on Supplementary Figure I-1-1B shows resulting cumulative curve (which represents a sum of all PET counts presented in I-1-1A. In this step of our algorithm, we extrapolated this curve for the large enough library size using the best-fit Hill function (1):

$$f(x) = \frac{ax^b}{c^b + x^b}$$

where x is the total number of slPET matched to the genome and $f(x)$ is the number of distinct PET fragments in the given sub-sample, respectively; the parameter a is the total number of ChIP DNA fragments identifiable by the PET approach; b and c are positive constants. We have shown that this model accurately fitted the growth kinetic curve for distinct SAGE tags (1) and ChIP-PET data (2). Figure I-1-1B shows that the growth function $f(x)$ fits the PET experimental data very well. All of the three best-fit parameters are highly significant ($p<0.0001$) ($a=447,932 \pm 41.7$; $b=1.01 \pm 0.0001$; $c=438,360 \pm 83.8$) and parameter a gives the estimation of total possible detectable distinct PETs to be **447,932**. Therefore, **~61%** ($273,566 / 447,932$) of the total cloned ChIP fragments were captured by current depth of sequencing.

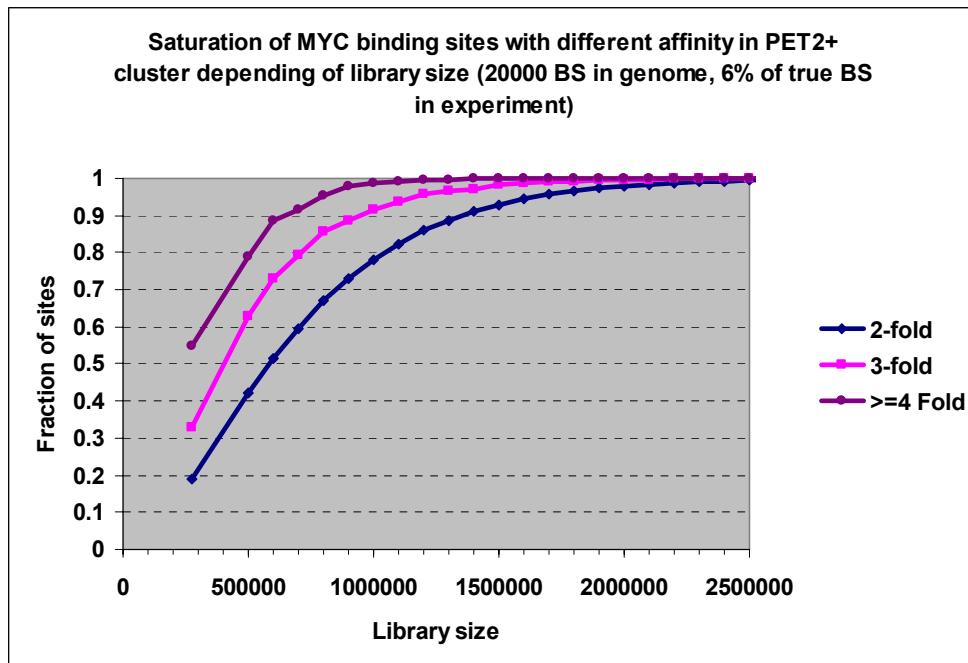
To estimate the sensitivity of the ChIP-PET method and the amount of sequence reads required to detect all the potential Myc binding sites on P493 genome, we use curve-fitting analysis. Three variable factors can determine the amount of sequencing reads required to reach certain detection sensitivity: 1) Total number of potential binding sites on whole genome; 2) The affinity distribution of these binding sites (depends on the transcription factor; represented by fold of enrichment); and 3) Fractions of sequence reads contribute to the true binding signal (relates to experiment design; correlates with antibody IP efficiency). By varying the total number of noise sequences (between 1-10 %), Monte Carlo simulation was used to predict the distribution of cluster size and numbers, and the predictions were fitted with experimental data derived in the current



library (Figure I-1-2, left). From the fitted curve, we found ~ **6%** of total sequences in the current library were derived from true IP enrichment. We next approximated affinity function by Pareto distribution using ChIP-qPCR results over 200 assays). The affinity

distribution of Myc-bound ChIP DNA is very much skewed with the majority of sites being relatively low affinity and only few sites being high affinity. With the affinity function, sequencing saturation level of the current library and 6% out of the total sequences contributed to the true binding, we estimate the total number of Myc binding sequences in P493 genome could be as large as 20,000. The following figure (Figure I-1-3) contains saturation plots of MYC binding sites with different affinity for library size up to 2.5 million sequences. As shown in the figure, if the number of PET sequences in this experiment increases twice to 500,000, we estimate to uncover 80% of the binding sites enriched by ≥ 4 fold in PET-2 clusters. With 1 million PETs, we can expect to identify more than 90% MYC binding sites with ≥ 3 fold enrichment within PET clusters.

Figure I-1-3. Saturation plots of Myc binding sites.

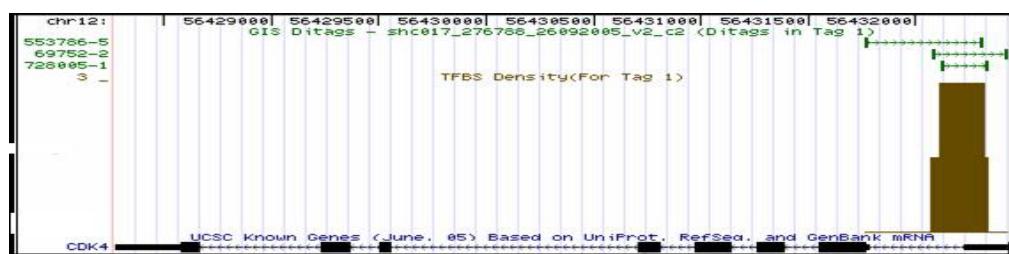


I-2. Using PET clusters to define Myc binding.

Example 1. CDK4 (Cyclin-dependent kinase 4)

PET-3 cluster location: chr12:56431764-56432434 (671 bp)

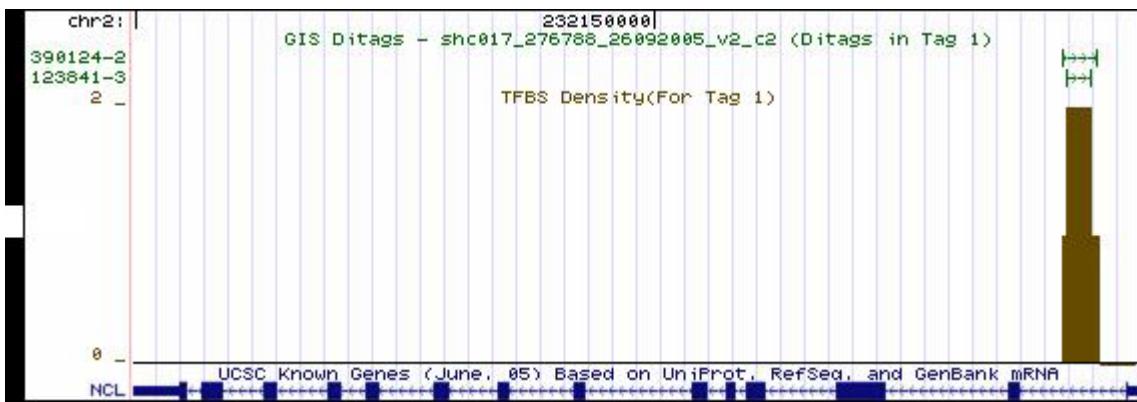
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CCATTCTCAGATCAAGGGAGACCTACAATCACAGACTCTATACCAAAAGTCGCTTACAGAGTTAGGATGGTATGAGCCTGCAGCAA
CAAAGGGACTCCAAAAAAAAGCGAAAGAACACCACCGATCCCATCCCCGCTCCAGTCTCCTGGGGCCGGCCCCAGAGATA
ACACAATGACTCAATACCAACCCCTCCAGCCACGTGAGGCCCTGCAATAGAAAACGCTTTCTGGACAATCGGCCCGCACAA
AGATCACACATGACACATGCCCTGCATGAAGATCCTACACCTCAGTCCCTAAATTATACTTCCCATGACCACAAAGGCCCACTTC
CCGCCCTTGAGCGACCCCTCCATAACCAGCTCGGAAACGAACCGCCTGGAAAGCTGTGAGGGGGCGGGCACTGTTCTCATTCTGGG
AAGGGACTGCACCTTACCTCACGCCAGCCGGGGTGTGCTGGGGCGGGCCCGTTATCGGGGCCCGAGCCGGTTCTACGGCCCCATAC
ACCCGAGCTCGGTCCGGAGCAGCTGGACGCAGAGGCCCGACCATAGACACAGGCCGAAGCTAGAGGCCCTCACCCCCCACCTA
CCATGTGACCAGCTGCCAAAGAGGCCGCGGAAACTGGGAGGGCGGG
```



Example 2. NCL (Nucleolin)

PET-2 cluster location: chr2:232153943-232154292 (350 bp)

```
TTTCCCAGCGAGACAACCCCGCCCCCTTAAAGAGGGCGGCCGGCCACGTGGGGGTACCTGGTAGGCCACCACGTGCCCGAAACACAGCGC
AAAAGGCACGCAGGCCAGAGCCACCTTCCGGGGCCACCACGTGTGGCTTGCAGGCCGGGGCGAGACATCCGAGCGCAGCCGGACTC
CGACTAGGGCGATAACCGCATTCCGGCCAAGGCACCCGGCTCTGGAGATTCCAGGACCCACGCCGGCGCCCACGTGGCAG
GCCCGCTCCCGGGCACGTGCGTCAGGAGTCGAGTCCAGCTCGTACCGTCCAAAAGTTGGTCTCATCTCTCACCCGA
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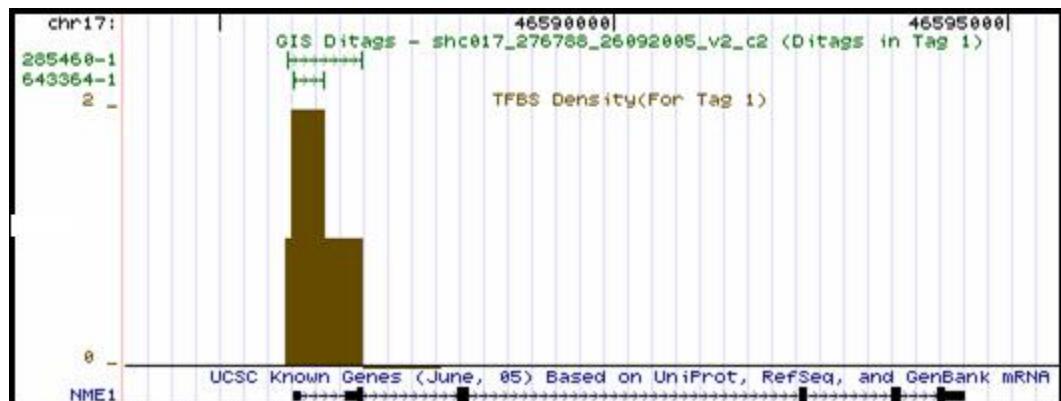
Example 3. NME1 (Non-metastatic cells 1, protein (NM23A))

PET-2 cluster location: chr17:46585830-46586802 (973 bp)

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AAGTTGTCCTAGAACGTGCTACTCCAAAGAGGAAGCGTGGCGAGCGGTGTTCTGCAAAATGGGCTCTCGGCA CGGGATCTGC
GCAGAACGCTCCGTGCGTCAAGTGCTGCGAACCACGTGGGTCCCGGGCGCGTTTGGGTGCTGGCGCTGCAGCGGAGTTCAAACC
TAAGCAGCTGGAAGGGTAAGAGGTGTTGGGATCTGAGAGAAAAAGAAAAGAGTGTAGTCGGGGAGTGGGTAGGTGAGGAGTTAG
TGAAGAGATGAGTTCAAGAGGCAGGGAGGATGGATGGGAGGGGGCAGGGAGCGCTGTGGACAAGTGCAGACCGGTG
GCGCACGTCCCACGCCACGTGGACTCGCCTTGTGGTGGCCGCTTCTCGTCAGGCCGCGACGACAGGGCTGTGCCTTATTGTGTC
TGTCGAGAGCAGTGGGGGACGGAGTTGGCGCTGTAAAGTGTTGCTGAATAATGACGGGTGTTGTGTCATTCAAGCAAGCA
CTGAGTGCTTACTGTTGTCACCGGGACCGATGTTGGAGGGACATTAGGGTGTATTCTGGCCTTAGTCCTGTTCTGGA
CAATTATGCTTGGCCGACCCCCATCGTGCAGTCTCCGAGTCTGGCTTGTCTCTCTCTTTTTGGAAAGTTGCG
AATGGTGATAATGATTCTTGCTCTATTGACTGCTAGGCGCTGTGGCTAGGTACCATAGAGTCTCACACAGGACTAAGTCAGCC
TGGTGTGCAAGGGAGGGAGACACACACAAAGAAAATTGGACTACAGTGCTAAAGATGCTGTAAGAAGAGGTTAAAGGACAGGAAGA
TGGGGCCAAGAGATGGTCTACTGTCTACTTAGGGATGCTTCAAGGGAGGGCCTCTATCTCAAGCTGTGATACA

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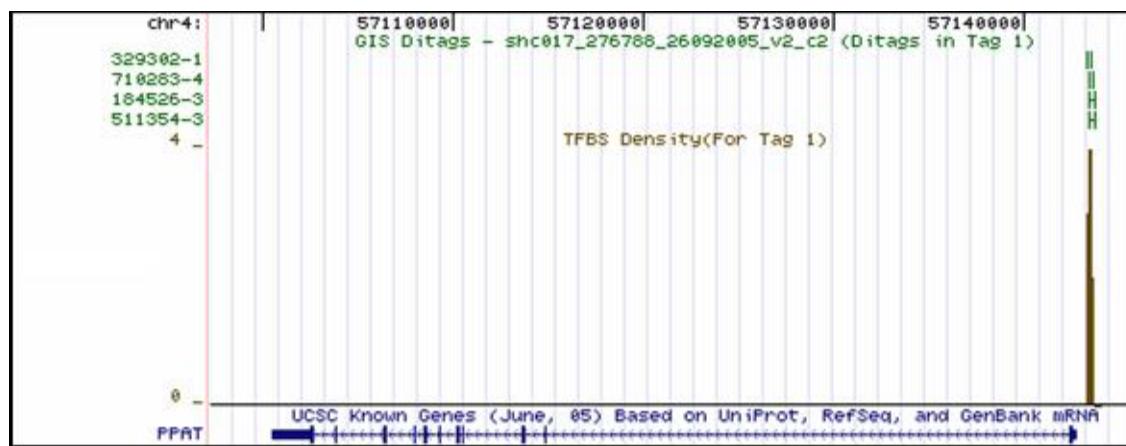
Example 4. PPAT (Phosphoribosyl pyrophosphate amidotransferase)

PET-4 cluster location: chr4:57143317-57143689 (373 bp)

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CCCGCCCCAGCGAAGCTCTGACCACCCCTTTCTAGAGTTCTGCCTCGCTCCGGCGCGTGCAGCCCTAGCCCACCTAGGAT
AATGGCGACAGCTGAGGGTGAAGTAACAGGGATCCGGGCCTTCACGGTCTCCCTGACCCCCAGGCCGTGAGCTCGGGCCACGTGCGAG
CCGCAGAAACTCTGCCCCCTCCCTGAGCAGCGCCTCTAGGCAGCCGCGGGCGCACACGTGGCCCAGGCCTCCGGGCTCCCCG
AACTTTACTGCCTCGGGATGGGGAGAAGGAGCAAAGTAGAGGAGAACGAGAAATGGCCAAGGGTGGAAAGGTGCCTGGAAGTATTAT
TTATAATCAATAGCTAT

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*Sequences shown are cluster regions with E box highlighted in yellow.

I-3. *De Novo* prediction of E-box using MYC ChIP-PET dataset

To attenuate the noise and ensure prominence of motifs relevant to the MYC ChIP, we took the sequences from 593 PET-3+ clusters (clusters containing a minimum of 3 overlaps) and masked the repeat regions annotated in the human genomic sequence from the UCSC genome browser (hg17). The masked sequences were fed into the motif discovery algorithm Weeder (3), setting HS (*Homo sapiens*) as the background genome, searching both strands, allowing multiple motif occurrences in each sequence, and running the most thorough search (i.e. analysis type = “extra”). The motif CACGTG (E-box) was found to be overrepresented in the sequences (Supplementary Figure I-3). From these sequences, a Position Weight Matrix (PWM) M was built to model the E-box.



Supplemental Figure I-3: *De novo* prediction of the Myc binding motif.

Sequence logo of Myc binding E box derived from Weeder algorithm.

The p-value (p) of a set of clusters (S) being enriched is computed in the following manner. Firstly, a collection of 10,000 random human coding sequences was selected to be the background set (B). A random set of clusters R was selected such that $|R| = k|S|$ where k makes $|R| \gg |S|$. Next, we use the background set B to calculate the appropriate PWM scoring cutoff T such that the false discovery rate is at most 1e-4. Then, we calculated the statistical significance p of motif overrepresentation in the set S against R , in terms of predicted sites per nucleotides, using PWM M and cutoff score T .

I-4. Validation of selected PET-2 and PET-1 clusters by ChIP-qPCR.

The 3 binding features (presence of E-box, proximity to a CpG island, and proximity to a transcriptional start site (TSS)) derived from 593 reliable PET-3 clusters were used as criteria to select specific PET-2 clusters from random noise. To assess the accuracy of the selected clusters with each binding characteristic, we first categorized all PET-1 and PET-2 defined regions with individual binding features (table below).

Type	Description of different category	Numbers of PET-2	Numbers of PET-1
	Total	11,000	248,980
1	Ebox	1320	10519
2	Within 5kb of CpG	1854	25314
3	Within 10kb TSS and 1st Intron	2212	27857
4	Ebox and within 5kb of CpG	436	2105
5	Ebox and within 10kb TSS and 1st Intron	377	1472
6	Within 5kb of CpG and within 10kb TSS and 1st Intron	1138	7239
7	All three	263	587
8	None of these three	7302 (66.4%)	195519 (78.5%)

We also used the same location features to scan hg17 genomic DNA for regions fulfilled all three criteria but were not covered by any PET sequence and found 3689 sites. 10 to 15 loci were randomly picked from each class for qPCR validation. The percentages of positively validated sites are listed below. As shown, all PET-2 and 70% of the PET-1 clusters located proximal to promoter, CpG and contained E box were validated as true Myc binding regions. Among the other 6 categories, E box containing clusters also display high percentage of positive validation. However, less than 20% of the genomic background with all 3 features was positively validated and these validated sites, in general, had low enrichment fold (see main text Figure 2B). It is evident that many of

the binding sites are represented by PET clusters due to their weak affinities and limited library sequencing.

	PET-2							PET-1	Genome PET-0
	Ebox	Promoter	CpG	Ebox & Promoter	Ebox & CpG	Promter & CpG	All 3	All 3	All 3
# of tested	13	15	23	11	12	10	14	10	11
Positive	6	3	7	5	7	5	14	7	2
Negative	7	12	16	6	5	5	0	3	9
% of validated	46.15	20.00	30.43	45.45	58.33	50	100	70	18.18

Note: 1. In each category, clusters were selected based only on the features described and were excluded if they also contain other binding characteristics.

2. Genome PET-0s were selected regions proximal to promoter and CpG and also contain E box but not covered by PET sequences.

I-5. Identification of cofactor motifs enriched in Myc binding regions

We intended to search if there are any transcription factors whose binding consensus sequences are enriched in Myc binding regions. 593 PET-3+ clusters were scanned separately by TRANSFAC 9.1 using a cut-off of 0.9 to minimize false positives. Known TFs whose motifs appeared in any of the Myc clusters are considered as candidate co-factors. To compute the p-value of the candidate co-factor present in the clusters, we first took 10,493 human CDS downloaded from UCSC as the background and calculated the number of occurrences of each candidate co-factor in such background using their PWM. The background is used to determine the cut-off threshold for matching against the PWM of a TF based on the e-value (0.0001). To obtain the cut-off similarity score threshold with the PWM of a TF, we computed the similarity score of all length-x substrings of the background sequences. We sorted the scores in descending order and use the similarity score at rank (0.0001 * number of length-x substrings) as the cut-off threshold.

To estimate the probability of the TF appearing in random, we next generated 100-fold random clusters of the same length distribution as the PET clusters. For each TF, we computed the number of matches with similarity score > threshold using its PWM in these 100-fold random clusters as well as 2 subsets of Myc PET clusters. This gives the probability of the TF appearing by random chance as p_r and TFs matches in Myc binding loci, n. Using a binomial approximation to normal $\sim B(n, p_r)$, we compute the p-value of the TF present in the original clusters. 20 TFs with p-value $< 10^{-20}$ found in 593

PET-3+ clusters were reported in the table (Table 1-5A) below. The significance of these 20 co-factor occupancy was validated by the 3703 selected PET-2 clusters compared with 7297 non-selected PET-2 clusters (Table I-5B). Based on the fold of enrichment and p-value analysis, all except one (HSF1) was still significant although half of them had marginal enrichment compared with 7297 non-selected dataset of PET-2 clusters. The fold of enrichment is calculated by comparing the frequency of occurrence in the test set with random occurrence on genomic background.

Supplemental Table I-5

A. Transcription factors found with binding motifs enriched in 593 Myc binding loci.

		Total clusters		Clusters with E box (157)		Clusters w/o E box (436)	
Factor Name	Accension	Enrichment Fold	P-value	Enrichment Fold	P-value	Enrichment Fold	P-value
AP-2 beta*	M00189	24.19	3.21E-308	61.64	1.59E-191	16.27	1.09E-146
E2F1	M00938	15.57	1.83E-199	36.97	7.28E-167	10.28	4.37E-116
Sp1*	M00931	15.07	0.00E+00	29.51	7.83E-202	12.02	1.31E-182
Muscle initiator	M00321	11.02	1.98E-132	28.19	1.37E-93	7.39	4.94E-58
c-Myc:Max	M00322	10.12	1.75E-180	58.02	7.52E-258	0.00	6.70E-35
Elk-1	M00025	8.42	1.68E-78	14.58	7.52E-58	7.12	8.25E-34
EGR*	M00807	8.00	1.76E-102	21.07	4.12E-114	5.24	6.05E-29
MAZ	M00649	6.58	4.96E-142	9.79	9.52E-71	5.90	4.97E-79
Sp3*	M00665	5.93	5.27E-79	7.23	6.52E-37	5.41	2.51E-46
COUPTF	M01036	5.60	1.30E-77	6.68	1.44E-34	5.18	9.28E-47
CREB*	M00917	5.28	9.19E-40	10.50	5.44E-11	4.17	9.59E-31
VDR	M00444	5.09	8.06E-72	8.70	2.46E-54	4.33	2.20E-30
PPARalpha:R XR-alpha	M00518	4.99	1.41E-50	7.52	9.84E-39	3.99	1.47E-21
p300	M00033	4.21	1.12E-45	5.46	7.00E-26	3.71	2.07E-24
LF-A1	M00646	4.12	1.11E-65	6.67	3.90E-50	3.59	1.07E-27
STAT3	M00497	4.08	1.50E-37	5.08	1.05E-19	3.68	2.68E-21
BSAP	M00144	3.91	3.37E-28	5.12	8.43E-17	3.43	4.52E-15
HNF-4 direct repeat 1	M00764	3.70	1.62E-29	3.80	3.16E-10	3.66	3.74E-21
HSF1	M01023	3.70	3.54E-27	3.67	8.12E-09	3.71	3.50E-20
ATF-1	M00691	3.41	9.91E-19	6.67	3.09E-11	2.72	2.25E-10

B. Validation of the co-factor occupancy in the selected PET-2 clusters.

Factor Name	Accension	3703 selected PET-2		7297 un-selected PET-2	
		Enrichment Fold	P-value	Enrichment Fold	P-value
AP-2 beta*	M00189	18.07	0	1.38	0.00967
E2F1	M00938	31.13	0	5.17	5.24E-241
Sp1*	M00931	11.71	0	1.54	1.05E-09
Muscle initiator	M00321	9.39	0	1.75	7.31E-13
c-Myc:Max	M00322	8.95	0	1.51	4.3E-10
Elk-1	M00025	6.09	2.00E-278	2.03	7.75E-24

EGR*	M00807	7.78	0	1.83	8.68E-23
MAZ	M00649	5.10	0	1.98	5.22E-66
Sp3	M00665	4.70	0	1.97	1.14E-46
COUPTF	M01036	3.95	1.82E-239	2.08	8.17E-64
CREB*	M00917	4.16	6.69E-160	2.11	2.85E-39
VDR	M00444	4.16	0	2.03	6.12E-67
PPARalpha:RXR-alpha	M00518	4.33	1.71E-261	2.17	4.04E-64
p300	M00033	3.86	9.50E-269	2.02	2.36E-67
LF-A1	M00646	3.77	0	2.05	2.64E-107
STAT3	M00497	3.44	5.07E-173	1.88	4.22E-45
BSAP	M00144	3.71	4.50E-176	2.03	1.01E-50
HNF-4 direct repeat 1	M00764	3.13	5.87E-133	2.01	1.99E-58
HSF1	M01023	2.69	6.37E-78	2.12	5.76E-66
ATF-1	M00691	3.41	3.77E-130	2.10	2.67E-53

I-6. Identification of motifs enriched in Myc binding regions associated with down-regulation

The co-factor motif analysis was performed on the 313 clusters of Myc-downregulated genes and 443 clusters of Myc-upregulated genes. Cluster sequences from these 2 groups were scanned by TRANSFAC 9.1 using a cut-off of 0.9 to minimize false positives. Each set of clusters generated a list of known transcription factor binding sites (TFBSs) found by TRANSFAC. Next, we combined the 2 lists of TFBSs, noting which TFBSs were present in both sets of clusters and which TFBSs were present in only the downregulated clusters. Taking human CDS as the background, we found the number of occurrences of each TFBS in the background using their PWM. Then, we generated random clusters of the same length distribution as the PET singletons. The probability of the TFBS appearing in random was calculated and used to compute the p-value of each TFBS in the 2 lists with respect to the DownRegulated and UpRegulated clusters. TFBSs that are found to be significant in the DownRegulated clusters (p-value > e-10) and not significant in the UpRegulated Myc clusters (< 0.05) were chosen.

Supplemental Table I-6.

Transcription factor motifs enriched in Myc binding regions of down-regulated genes

	Down-Regulated subset (313 clusters)	Up-Regulated subset (443 clusters)		
TF motif	P-value	Match	P-value	Match
NERF_Q2	1.66E-21	31	1.96E-06	36
EBF_Q6	4.48E-19	42	1.26E-01	28
ZIC3_01	5.52E-15	48	1.13E-07	43

MZF1_01	6.78E-15	55	1.73E-07	65
LFA1_Q6	5.91E-14	67	3.61E-07	72
MYOGENIN_Q6	1.65E-11	60	2.19E-04	73
NF1_Q6	8.62E-07	30	1.00E+00	21
RFX1_01	1.29E-05	29	1.84E-01	50

I-7. Functional gene categories associated with different cofactor motifs

We sought to categorize the function of the target genes using EASE (Expression Analysis Systematic Explorer) analysis based on the enrichment of different combinations of transcription factor binding motifs within in the binding clusters (4). We observed different types of gene functions tend to associate with binding sites with specific transcription factors (Supplemental table ST4). For example, targets enriched with Sp1 sites appear to have an over-representation of genes involved in ion transport such as ABCC4, ATP2A2, ATP5D, ELP3, KCNC4, KCNJ6, KCNQ5, OPLAH, SFXN4, SLC16A6, and TCIRG1 (EASE score $p = 0.0025$). Targets with AP-2 motif are over-represented with genes involved in ribosomal structure and biogenesis such as DKC1, EIF3S9, EWSR1, G3BP2, PUM2, RPLP2, RPS2, and RPS20 (EASE score $p = 0.014$). Target genes with the MAZ binding motif are enriched with genes involved in signaling and development such as ATP2A2, BMI1, BRD2, C15ORF2, CHST8, DDX1, ID3, KIAA0922, MDS032, MFNG, MPZ, NKX2-2, NOTCH1, PIK3R1, PRM1, SPIN, TRAF4, and TUBB4 (EASE score $p = 0.022$). Target genes in this dataset with EGR1 sites do not appear to be enriched in a specific functional category, whereas those with E2F1 sites are enriched with nucleic acid binding proteins.

I-8. Comparative Analysis of Myc binding targets found from different studies

Up to now, three independent large-scale studies on Myc binding were reported in different cell types by different methods. In order to evaluate dynamic nature of Myc binding in different cells and condition, we sought to determine the common vs. unique binding sites; particularly the degree of overlap between binding loci identified in this study and others. These overlaps may signify Myc binding regions that are independent of specific cell types or culture conditions. The first report was from Ren and his colleagues (5). 876 Myc binding sites associated with promoters in the Daudi Burkitt's lymphoma cell line were identified by employing ChIP-on-chip using promoter PCR

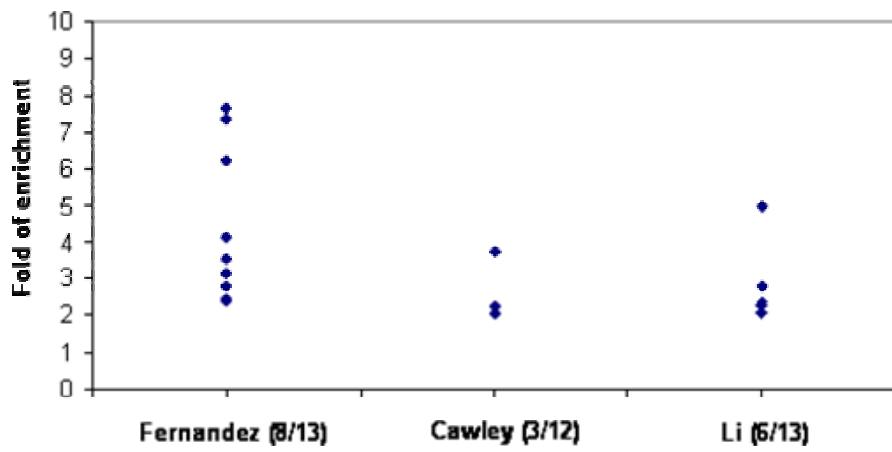
arrays. Fernandez et al (6) selected promoter E box within 2 kb of each side from transcription start sites of 6541 Genbank entries and tested them for Myc binding by ChIP-qPCR from 5 different cell lines. Among all the positive binding sites reported, 139 high affinity sites were found in the same P493 cells used in this study. The third Myc binding study identified 756 Myc binding loci on Chromosome 21 & 22 by oligo tiling arrays (7) in Jurkat cell line.

As shown from the comparison table below, only limited overlap was shared between these datasets and PET identified loci. ~ 0.79% to 3% of sites found by these reports were identified in our 593 PET-3+ clusters. When we expanded the comparison using all loci defined by PET-1+, the shared sites increased 17.46% to 44.06%. Among these 3 studies, the Myc binding promoters defined by Li et al using promoter array displayed the most overlap and genomic binding regions on chr. 21 &22 showed the least.

	Fernandez (promoter E box)	Li (promoter)	Cawley (Chr. 21 & 22)
Total sites	139	876	756
Overlapped with PET-3+	4 (3%)	19 (2.17%)	6 (0.79%)
Overlapped with PET-2+	22 (16%)	107 (12.21%)	27 (3.57%)
Overlapped with PET-1+	47 (34%)	386 (44.06%)	132 (17.46%)
Non overlap sites	92	490	624
Total no. validated	13	13	12
Positive	8	6	3
Negative	5	7	9
Positive percentage	61.54	46.15	25.00

One reason for the lack of significant overlap could be the sensitivity of different methods. As only up to 61% of cloned fragments were sampled by current sequencing, it is possible that ChIP fragments derived from the non-overlapping binding sites were yet to be sequenced. A subset of them was selected from each dataset and tested by ChIP-qPCR in our P493 ChIP DNA. The result showed between 25% to 62% of them were validated positive, and consistent with the experimental system used, Myc bound E box in P493 cells have highest validation positive rate and sites detected by chromosome tiling array were least validated. As expected, >80% of the validated sites were less than 5 fold enrichment, indicates these are low affinity Myc binding sites missed by our current ChIP-PET sensitivity (Supplemental Figure I-8). The remaining sites, which failed to be validated, could result from false positive noise in other detection methods, the antibody IP variation or dynamic Myc binding in different cells or experimental conditions. It is noteworthy that, while interactions between Myc and its targets are

highly complex and dynamic, all studies done so far have only partially captured a snapshot of Myc occupancy on whole genome. The functional core Myc targets can only be revealed when we have a comprehensive and saturated coverage. Despite the current limited scale, when we intersected all 3 datasets (Li, Fernandez and the current study), 15 genes (Table I-7) are commonly presented in all studies and 10 of them including ATF4, BLK, HNRPA1, NCL, MCM4, NME1, NR1D1, and TRA1, were regulated at the expression level and bound by Myc.



Supplemental Figure I-8. ChIP-qPCR validation on non-overlapping sites.

Supplemental Table I-7. Common Myc binding targets identified by 3 different studies

Known Gene Target	E box hit	Distance	Binding Location	Gene Function	Fold change
ATF4	TRUE	219	5'	regulation of transcription	Up
BLK		2080	5'	intracellular signaling cascade	Down
HNRPA1	TRUE	307	5'	mRNA processing	Up
HRSP12	TRUE	168	5'		Up
MCM4		303	5'	regulation of transcription	Up
NCL	TRUE	445	5'		Up
NME1	TRUE		1st intron	nucleotide metabolism	Up
NR1D1	TRUE		1st intron	regulation of transcription	Up
OPRS1	TRUE		intron		Up
PPP1R7		69	5'		
RPL19	TRUE	0	5'		
RPS19		0	5'		
TCF12			1st intron		
TRA1		952	5'	protein folding	Up

II. Supplemental Tables

Supplemental Table ST1. PET and PET clusters distribution along on human genome.

Chr	Chr. Size (mb)	Chr. Size (mb) [Masked]	PET	PET density (PET/mb)	PET density (PET/mb) [Masked]	PET- Clusters	Cluster density (Cluster/mb)	Cluster density (Cluster/mb) [Masked]
1	222.828	114.617	22330	100.21	194.82	2297	10.31	20.04
2	237.503	128.039	23160	97.51	180.88	2165	9.12	16.91
3	194.636	101.464	19386	99.60	191.06	1780	9.15	17.54
4	187.161	96.08	17425	93.10	181.36	1491	7.97	15.52
5	177.703	92.653	16979	95.55	183.25	1507	8.48	16.26
6*	167.318	88.726	10605	63.38	119.53	792	4.73	8.93
7	154.759	80.619	14338	92.65	177.85	1365	8.82	16.93
8	142.613	74.057	13959	97.88	188.49	1266	8.88	17.09
9*	117.781	61.084	16116	136.83	263.83	2060	17.49	33.72
10	131.614	70.302	12892	97.95	183.38	1334	10.14	18.98
11	131.131	67.074	12986	99.03	193.61	1303	9.94	19.43
12	130.259	65.815	12821	98.43	194.80	1206	9.26	18.32
13	95.56	52.019	9320	97.53	179.17	823	8.61	15.82
14	88.291	45.956	8925	101.09	194.21	848	9.60	18.45
15	81.342	43.139	8143	100.11	188.76	784	9.64	18.17
16	78.885	40.353	7771	98.51	192.58	926	11.74	22.95
17	77.8	40.979	8380	107.71	204.49	945	12.15	23.06
18	74.656	41.253	7575	101.47	183.62	782	10.47	18.96
19	55.786	23.963	5917	106.07	246.92	768	13.77	32.05
20	59.505	30.618	6603	110.97	215.66	719	12.08	23.48
21	34.17	18.502	3778	110.56	204.19	512	14.98	27.67
22	34.765	18.135	3803	109.39	209.70	486	13.98	26.80
X	150.394	61.745	12881	85.65 (171.3)	208.62 (417.24)	1109	7.37 (14.75)	17.96 (35.92)
Y	24.872	9.537	517					
Total	2851.332	1466.729	276610		188.59	27268		18.59

* Note that P493 cells are monosomic for Chromosome 6 with a small ring Chromosome 6 and trisomic for Chromosome 9 (unpublished data).

Supplemental Table ST2: PET clusters associated with 24 previous known Myc binding loci.

Gene target	Regulation	Previous binding evidence	PET cluster size	Cluster location	Relative to Gene	Distance	E box	Relative to previous known binding site
APEX	U	C	1	chr14:19993160-19993247	5'	40	E box	overlap
CAD	U	C	1	chr2:27351972-27352281	5'	0	E box	overlap
			1	chr2:27354527-27354751	1st intron			
			1	chr2:27371973-27372356	intron			
CCNA2	U		1	chr4:123102019-123102418	5'	0		
CCND2	U	C	2	chr12:4194938-4195416	5'	57976	E box	Not overlap
CCNE1	U		1	chr19:34999208-34999412	intron			
CDK4	U	G, C	3	chr12:56431764-56432434	1st intron		E box	
CDKN1A	D		2	chr6:36750555-36751490	5'	3403		
CDKN2B	D	G,C	2	chr9:22027531-22028070	5'	28368		Not overlap
CHC1	U	G	4 singletons		intron		2 E box	
DDX18	U		2 singletons		intron		E box	
DUSP1	D		1	chr5:172130603-172131167	5'	81	E box	
			1	chr5:172129835-172130315	1st intron			
EIF4E	U	G, C	2	chr4:100101519-100101844	3'	56560		Not overlap
ENO1	U	C	2	chr1:8872342-8872815	1st intron		E box	Not overlap
FASN	U	C	2	chr17:77649758-77650290	5'	752	E box	overlap
FKBP4	U		1	chr12:2775748-2775923	1st intron			
			1	chr12:2762654-2763040	5'	11565		

FN1	D		2	chr2:216176395-216177099	5'	50225		
GADD45A	D		1	chr1:67863354-67863579	1st intron			
HSPA4	U	G	2	chr5:132490368-132492798	3'	23883		
			2	chr5:132485266-132485973	3'	17383		
HSPCAL3	U	C	2	chr11:27891505-27892175	5'	22394		Not overlap
			2	chr11:27806313-27806606	3'	61721		
HSPD1	U	C	1	chr2:198190094-198190386	5'	184		
HSPE1	U	C	1	chr2:198190094-198190386	5'	311		
LDHA	U	G, C	3	chr11:18371314-18372534	5'	687		
MGST1	U	C	2	chr12:16328837-16329224	5'	62938		Not overlap
MYC	D		4	chr8:128819877-128821548	intron		E box	
NCL	U	C	2	chr2:232153943-232154292	1st intron		E box	overlap
NME1/NM23A	U	C	2	chr17:46585830-46586802	1st intron		E box	overlap
NEM2/NM23B	U	C	1	chr17:46598731-46599031	5'	13		
NPM1	U	C	4	chr5:170747835-170748452	1st intron		E box	
ODC1	U	G, C	1	chr2:10539109-10539583	5'	328	E box	
PPAT	U	C	4	chr4:57143317-57143689	5'	544	E box	
PTMA	U	C, D, G	2	chr2:232397421-232397994	5'	1137	E box	overlap
RPL23	U	C	2	chr17:24070343-24071822	5'	201		overlap
RPL3	U		2	chr22:38002328-38002788	3'	30959		
RPL6	U		2	chr12:111313488-111314051	5'	3442		

RPS15A	U		1	chr16:18708871-18711840	5'	2413		
SRM	U	C	1	chr1:11054445-11054737	5'	268	E box	
TERT	U	G, C	1	chr5:1347555-1348150	1st intron		E box	
TFRC	U	C	2	chr3:197252295-197252540	3'	12045		not overlap
THBS1	D		1	chr15:37659499-37659653	5	1062		
TNFSF6	U	G	2	chr1:169344040-169344543	5'	15513		
TP53	U	G	1	chr17:7531509-7531709	5'	84		
TPM1	D		1	chr15:61118232-61118484	5'	3643		

U, upregulate; D, downregulated; G, gel shift; D, DNA footprint analysis; C, ChIP analysis.

Supplemental Table ST3: List of primers used in ChIP-qPCR validation

Cluster Location	Cluster Overlap Count	Known Gene Target or Binding feature	ChIP primers Forward	ChIP primers Reverse
chr5:176671494-176672106	4	MXD3	CATTCCGACATGGCTTCTCA	CCAGCCAATAGGCATCAGA
chr8:109329769-109330175	3	EIF3S6	TGAGCAAGGCCGAAAGG	CTTAACTGAGACGACGCTAACTACC
chr7:44798312-44799588	5	MYO1G	CCACCCAGGTATGCAGAA	ACTACACGTGCTACTTCCTCTCAAGA
chr4:57143317-57143689	4	PAICS	AGCCCTCAGCCCACCTAGGA	GGGTCAGGGAGACCGTGAA
chrX:153554735-153555905	4	DKC1	TGTTTTCTCGCTTACCTACGGAT	AAATCGCCTAACGACCCATTTC
chr6:41783220-41783946	3	TFEB	CTGTCACTGCGCCTGC	ACGAAATTACTCCCCCACC
chr5:170747835-170748452	4	NPM1	CTCGTGAGCCAGGGATGCT	CCCTAGTGCTACCAGCCTCTAAC
chr15:97010778-97011620	4	IGF1R	GGGTCCCCAGTTCAGAGG	CCACCAACGCACACTCG
chr16:11916365-11916879	3	GSPT1	CCCAAAGACCCGGACC	GTAACTGCGGACTCCAGAGC
chr22:18479043-18480456	7	RANBP1	CGTCTCTATGATCCTGGCTTCTG	CGCCTCTAGAGCTGGCTAAAGT
chr7:5821602-5822294	3	JTV1	AGGTCGACTTCGTGACGTCAA	CAAAGGCCAACGCTCAGAAA
chr22:30350977-30351708	3	PISD	CGCGGACAAGGTTGAGC	GAGATAAGATGTGGAGGAAGTGAGC

chr14:66043657-66044157	3	GPHN	CAGGTGGAACACGTTCTCGTT	AGGGCAGCTGGAGTGGAGAT
chr22:30474085-30474488	3	DEPDC5	GGAGCTCTGACGGATCTCGT	GTTCCGACTCAGTGATCTCCC
chr9:128981268-128981871	4	PPP2R4	TGGCCGCTGGTTGCA	TCCAGGTCCCCAGTGAGCTA
chr12:56431764-56432434	3	CDK4	GAGCGACCCCTTCATAACCA	GGGCTGGCGTGAGGTAAGT
chr10:112022749-112023631	3	MXI1	TGCAGGAGTGTGTGTTGGGA	CATGAGCCACATTCTCAAAGCT
chr6:33045270-33046164	4	BRD2	GCTCGGGACCTGGAATGATT	TTCCCTCCCCCGCAGTAC
chr1:155792567-155793804	3	IFI16	CCCTTGCCAGGAAACTGTT	GCTGACTAGTGCTGGCTTGCT
chr19:52795036-52795733	4	ZNF541	CTCAGCCGCCCTAGGATATTG	GGCGGGAAAAACCACAGA
chr18:58959991-58960414	3	BCL2	TACGCCAAAATGGGAACTGA	GGCCCTCCACGTTAATAATG
chr17:7096154-7096766	3	DERP6	CACCTCTCATCCAGACTATGTTAGG	GCCCTCTGATGGCGTCAT
chr20:33793360-33794031	3	RNPC2	TCTCTCCGAACACGAGCAC	CGCAACGCCCCGTACCT
chr13:29917696-29918274	3	HMGB1	AGCTGTCGGTGCATTGCA	GCTCCCAGTTTCCGGTAAT
chr11:18371314-18372534	3	LDHA	TCCAGCCTGGGTGACAGAGT	CATCTCATCTCGAGTCTCAACCA
chr7:89894708-89895548	3	PFTK1	GGCAGAAAAGGAATGTCCACTG	CTTGTGGATGCAAACCTCCC
chr9:90681065-90681456	3	SYK	CCTTGCAGTGAACCAGTGATT	CTCAGTGTCAACGACCGATGTG
chr6:31806358-31812270	3	CLIC1	GCTGGGCCCCACTGT	GTGCAAGTTCTAGCAGACTAAAGGA
chr8:128819877-128821548	4	MYC	TGGGCGGCTGGATACCTT	GATGGGAGGAAACGCTAAAGC
chr17:2243552-2244177	2	MNT	CGGGCCCCATACCTGGAT	TGGATGACAAGAACGCTCCAAT
chr19:54692223-54692858	2	RPS11	ACGCCCCCTGGCTTTAAG	AGAGGATCCGCCCTCGAAT
chr14:64638465-64639281	2	MAX	GGGCAGCCGAGACTTGTAGT	GGATTGTAGTTTCTGGAGCTACC
chr3:102887730-102888329	2	RPL24	ACAGCTGACCCCTGCAACA	AGCTGTCGCCATGAAGTAAGC
chr9:136699620-136700334	2	NOTCH1	CCTCCCTGGGTAGAGGCTAGA	TGCCCAGCTCATTCTTAGCA
chr12:4194938-4195416	2	CCND2	TCAGTAAATGGCCACACATGTG	GGAGCTCTGACGTGGTCAA
chr15:42621703-42622094	2	EIF3S1	TGTTAGTTCCTAGGCTGGCTATAGG	GTCACATGCAATGAGAACACATTAG
chr5:17285183-17285640	2	BASP1	CCCAAGGTAGAGTCCGAAATGA	GACAGACGAGGAGTGTAAACCAA
chr1:64023945-64024256	2	ROR1	TTCGATAACCTCAGCCCCAAGA	TCTGGTTGGGAAACCTACATCTATCT
chr3:170355988-170356439	2	EVI1	CCCATTCTGCTTGTGTTCC	TCCTGAACGCTGTCAGTGTCA
chr15:54999340-54999951	2	TCF12	AGGCAGCGTGAACCTCATCT	AAATGACCCCTCTGGCATTAAA
chr21:42599667-42600732	2	TFF3	GCTGTTGCCAGCCAAATTG	TTTACCTGCGTCTGGCTTCA

chr15:29109755-29110096	2	TRPM1	GGGCCTACATCCCCAGAA	CCATTTCACATAGCTACCCATT
chr21:39672449-39678307	2	WRB	CGGGTCTGGCGTAGGTACAG	CCCTAGAACCCAGAAAGTCTGATT
chr6:43650905-43651496	2	XPO5	TTAGTGCAGGAGAGACCATAAAGAAC	CTCGCTCTGTGCACTTTGTC
chr19:38855935-38856814	2	CHST8	AGTGACTTGCCTGGCAGGAT	TGTCTGACCTCACTGTCTACACA
chr8:11008970-11009262	2	C8orf5	AATGAACAAATGAGCATGGAATGA	GCACCACTCCATTCAAATAGGA
chr3:109497097-109497540	2	HHLA2	GGAGTTCCCCAAATGTACTTGC	AGCACACAAATCCCCTGATCA
chr1:151199868-151200490	2	IL6R	AGGTATTGCTCCAGGGACACA	CAGCTCTGGGCCTCAATCT
chr1:115576811-115578179	2	NGFB	GAGGCTATAAATGCCCTCTGACA	GTCCAACCTGGGTTCTAAGG
chr10:43031988-43034490	2	RASGEF1A	CCACCTCCAGCACCTGCTT	GTGCCGATGCCATCAGAAC
chr11:75038729-75039543	2	MAP6	ATCTGTCATTACACTGCTCATTCCA	AGAGAGCAGTCACTCAGGAACA
chr8:145918539-145918931	2	ZNF251	TGAATAAGGCTGGAGCTTCGA	GTGTAATGAATGTGGAAGAGGCTT
chr19:39483186-39483707	2	KIAA0355	CTGGATGCCCTGAACGTCTT	GCTGTGTGGCTGCCTTGA
chr11:107284917-107285737	2	SLC35F2	CCCTAGGAAAGACCAAACCAAGAA	ATGGCGTCATGTCTGAGCATAA
chr10:70516553-70516904	2	PRG1	ACCATGCCAGGGAAAATG	GAGGGAGAGGTTGTCCTCACAGT
chr11:104411124-104413067	2	CASP1	AATCAGAACTGTAGCCTGCATCAG	TTACTCTCCAAGCCCCATTCC
chr12:15784093-15786121	2	EPS8	TAAGGATAAAAGCATGCTCAAAGAA	AAGATTGTGCATCTAGGAGTTGATT
chr11:32068396-32070199	2	RCN1	CCCTGAGGACAACCAGAGCTT	CGAAGGTCTGGAGTCCTCCTT
chr13:26723697-26725643	2	RPL21	TTCA GTG GGT TTT TATT CCA A	TCACACCTGTAGGCTTCACAGAA
chr17:52517008-52517630	2	AKAP1	TGGTTGACCCCTTCGAGACAAG	TACAGCAACCGGAGGAACCT
chr3:38041007-38041864	2	PLCD1	TGAGGCGAGAGCGAAACC	ATGGCCCAGCCTTTGG
chr8:95981252-95982982	2	CCNE2	GGCACCTGCACCTCATTCTC	AGAACAGGGCAAGACAGCTTC
chr9:35062660-35063360	2	VCP	CTGACACTTCTGCTCCTCTCAA	AAGCGCTGAGAAACTGCAAAG
chr8:23441213-23441697	2	MSCP	GATCCAGCTTCCTGACCGAGAA	CGGTGTTCCAGGGCTTAAGA
chr19:40824584-40825275	2	ETV2	TGCTCTGACGTCTCGAAAAA	GGGTCTCAGCCCCATTCA
chr1:201523964-201525452	2	NFASC	GGTGATGAGGACCTGCAGACA	GAGGGAGGGATCCAGGAACA
chr17:46585830-46586802	2	NME1	AGCTGGAAGGGTAAGAGGTGTC	TCCTCGCCGCCCTCTAGAG
chr1:210843215-210843714	2	SMYD2	CCTGCACTGCACGTTTCAG	CACGCCCGGGTTGC
chr3:99173165-99173681	2	MINA	CTCCCCACACACCTGAACCTC	CGCCGGCGTCATGT
chr21:26464177-26464530	2	APP	GAGCGAAGGACTGGCTTAGG	GGGAGGCGAGAGACATTCA

chr3:52695278-52695609	2	GNL3	GGTTGAGGCCAATATTCCTT	TGAGTCTGGAGGCATTCT
chr19:2928074-2928549	2	TLE6	CCAAATTGCCTATAGCTCTGCAA	CGGGAGCCTCTGCTTACC
chr19:10673058-10673547	2	QTRT1	TGGCCACTCCTGTGTTCATG	CTTAGACCCAGATGGTAGGTATTGC
chr19:49942816-49943487	2	BCL3	ACCCCCAGCCCCTTAGAC	TCTCCCTCCCCCTTCCATCT
chr11:73371930-73372329	2	UCP2	CGGCCTCGCTGTCGATT	TGTTGCTGCAGTTCTGATTGG
chr22:38240529-38241011	2	ATF4	CGAAGGAAAGAACGGACTCTGA	TGGCCTCACGAAAGGAGAGA
chr5:139473064-139473833	2	PURA	CAGGCCCTCCTCCTACATC	GAGAAGGAGTCTGCCATACTAAGCA
chr17:35517897-35518426	2	NR1D1	TTCCCTCATCTGCCTCCTGTT	ATGAGCGAGTTGTTGTGGTAGAAA
chr17:1614316-1614758	2	SERPINF1	CGGGTGGAGACCAAGCTGTAG	CATGCAGGGAGAAAACCTTCG
chr13:77427645-77433599	2	EDNRB	TGCACGTACACTTCATGTGGTT	CCAAAGTCGTGAATGCTGTGA
chr21:44111109-44112179	2	AGPAT3	GGCCGCCTTAGGCTTACAT	GGGATAGCATCCGTGGACTTT
chr22:23881700-23883341	2	AB051458	CACTGGACAGAGCGTGTGT	TCCAGAAGTGTGTCCCAATCC
chr12:102479490-102481524	2	STAB2	TGTTACCCAGGAACCTTCCAACA	TTGGGTGACAGGAGGAATTTC
chr9:91642035-91642814	2	ROR2	TGTGGCCCTCTTCTGT	GGAAGCTGATCTGCCTCGAT
chr8:38504610-38505175	2	FLJ43582	ATGAAGCGTGGTGCCTTTA	GTGCCAGAGTGACAGTGGAA
chr11:35343612-35344240	2	SLC1A2	GTGGACTGGCATTACAGTTATATG	GAAATAATTGTGGATGCCTCGAT
chr21:39609227-39614375	2	C21orf87	TGAACAATGCCAGCTCTCA	GGCCTGAACTAAGTGGAAAT
chr12:106294106-106294752	2	AK124835	ACAGAAAGCCTGATGCATCGA	ATAAACACCAGGCTTCAGGAAACA
chr1:8872342-8872815	2	ENO1	GAAGGGCCTGGCCTGAGT	GGGAGTTGGAGTGGAGTTG
chr22:40666565-40667148	2	C22orf18	TGGGCTCGGAGTTAGCA	GCCTCCGAGCTGAAGGTGTA
chr22:43979457-43980660	2	UPK3A	GGGTGGCATGGTAACATG	CTGAGAGCAGATGCTGCAATG
chr19:627521-629775	2	FSTL3	TTCCCACCTGGTCGATAATG	GAAGGTCCCTGGTGTGGACAT
chr21:43356069-43359265	2	CBS	GAGGGTTCTGTGGGATTCCA	TCCTTGACGTGTACCTTATTCTG
chr3:185589096-185594267	2	CHRD	TTCACTTGCCTTGGCAACT	CCAAGTGGTTATCCCCATCCT
chr4:8203968-8204443	2	ABLIM2	AAGCCCTGGCTGGAAGAG	TGAAGAGGCAGGAAGGGATGT
chr21:44564693-44566690	2	PFKL	TCCCTCCATGGACATCTTG	GGGTTCGTGGAGACCAGGTT
chr12:48009208-48010226	2	TROAP	TGGGACTCAGGCTGGTCTT	CCAGAACCTCCAGTGACCTT
chr9:124699801-124700780	2	RPL35	CGCATGGCACGTGTCTTCT	CCCCCTTAGCTGCTGCAGTA
chr9:136669666-136672842	2	NOTCH1	ATGGGAAACACCCCAAGGAT	CACCTGCCTCTCTCCCCCTAAG

chr1:27117018-27117513	2	SLC9A1	CCCTCAGAGAGGAAGTGAGAGATC	CATGGGTTCCACTCACATGTG
chr3:152648730-152649121	2	IGSF10	CTGTGTCAAAACTATCAGCCATCTG	TGAGAGCCCCATTGTCAGTGA
chr1:4760433-4764347	2	SHREW1	AGCTGATGGCATGGCTCTG	AATAGACTGCGGAGGCAACAG
chr10:115364062-115364626	2	NRAP	CCCGCACTGGAGGAAGGT	AGACCCCTGGGCAGATGAAATG
chr21:31740280-31749673	2	TIAM1	GGCAGGTTGGTGAGAGGAA	AAGAGGCAAGGCCAGTTACG
chr1:110749253-110749770	2	KCNA10	GTGGAGGCTCGGCCAAT	CACATCCACACCTGGTCTTGT
chr1:162376890-162377607	2	ALDH9A1	CAAACGACAAACACAGGGAAA	ACGTGGCCCAAGGAACAAC
chr1:15587982-15593387	2	CASP9	TCAGAACTAGACGCACATGCAA	CGACTCATGCTGGTGGACAT
chr10:128914291-128919681	2	DOCK1	TTGACTCTTCTTCCCCATTGC	CCAGGATGGAAAATCGTTTG
chr1:3304188-3306258	2	PRDM16	CCGGCAACAGCCTAGTAATGA	CCGGCAGCAAATAACTATGCT
chr1:209246780-209247940	2	SNFT	TTCCCTTCTGTTCCCATTCTTG	CTCCCCATCCTCCAATTCTCT
chr19:53832600-53833291	2	CA11	GGGCGCCGCTTAAAGG	CGGAAACCAATTCCTCTTCT
chr5:52131707-52132296	2	PELO	GCCATGAAGCTCGTGAGGAA	CGAGGTTGTAAGTGTGCCACAT
chr11:63828303-63828817	2	KCNK4	CAGGGACCACCTCCTGACTAAGG	CGTTTTAATTACGTACAGCCTCTT
chr22:20321300-20322211	2	SDF2L1	CATGTGCTTACGGGCAAGAA	GGCTCACCTGGTTGTTGGA
chr21:44048490-44049598	2	D21S2056E	TGGGACCAGGAAGGACCTCTA	AATGCAGCAGGGCTTGG
chr15:68175161-68175705	2	TLE3	ACTTCCCGCGAGCCAAAG	AGCCAGCGTCAGGGCTCTA
chr17:39373601-39374162	2	PPY	CTCCCCATGCATTTGGCACTT	GCTCCCACACAGGCTCAATAA
chr1:143868141-143868439	2	PRKAB2	TCCCCGATAAAATCCCTTAATT	TGCAGCGGGTTGATTTCTG
chr11:803363-804001	2	RPLP2	GGGTAATCAGGGCTCTGCTTTG	GGCTCACTCCTGCATCCAT
chr12:115946712-115948398	2	TSC	TGCCCGTGAGCATGAAT	GGGCTGTGGGAACAATATTTG
chr15:41873228-41874429	2	SERF2	CGCTTCCCTTGACCTCAAAA	CCCAGAACCAACAGAACAAACC
chr21:45662916-45664287	2	C21orf123	AGGCCGCCCATCACTGT	TAAATCTGCTGAGGGAAACACTGT
chr10:102314146-102314480	2	HIF1AN	GTAGGTGTGAACATGCCGTGAGAGT	CCCTCCTGTGTCGTTCTCCT
chr11:67963632-67964319	2	LRP5	GCACATTCCAACAGGACACA	AAGCCGCCAACAGACA
chr8:146025673-146026611	2	ZNF7	GCAGGCCAAACGCTCAGA	GGCTGAACCCCCATGACATG
chr7:97144623-97145355	2	ASNS	CGCTGCTTAGTGAATCCCTGTA	TGCCCTTTGTTCTCCCTTTT
chr6:43001190-43001935	2	PTCRA	TACCTCCCTGCGTCACACT	GCCCCTGTAACTGGGTGGAT
chr6.97452217	1	PET-1with 3 criteria	CGTCCGCTCGGTTCTAG	CCACGTGCGGCCTGAA

chr14.74587352	1	PET-1with 3 criteria	TCTGCTGCTTCTAAGCTAATGCA	GCGTCATCAGGAAATCATTGG
chr9.125042428	1	PET-1with 3 criteria	GGGCAGGGAGTCTGAATCTTT	AACAGGCTGATTGGTCAAAGT
chr11.57265437	1	PET-1with 3 criteria	CCAAGCTTCCCTCCCTTGA	GGAAACTGGGCAACGAAGAG
chr16.30325800	1	PET-1with 3 criteria	CGGTAGCTGGGTGGATGTT	TGCCGTCTTCTCCATCTTC
chr2.27346207	1	PET-1with 3 criteria	ATCACCCCTCACCCCTCGTTCTT	TCCGGCGTGGGTCTGA
chr17.70660363	1	PET-1with 3 criteria	TTTCCCATGCTTCCTCCTAAG	AAGACACGTGAAATAGCCATATCTCA
chr8.116733584	1	PET-1with 3 criteria	CACGTGAGAGATGCAGTCAGATG	AAGGCGCCTCTGTTGTTGA
chr5.170225609	1	PET-1with 3 criteria	GCCCCCAGCCTACCCTATT	TCTGGCCTTGCTCTGAAAG
chr10.133967308	1	PET-1with 3 criteria	CCTCCCTGTCTGTCAGTCTCT	TGTGGCCGCTCAATTGGT
chr15:39592824-39597823	0	Genomic background	TTCTAGTTCCAGCCGTAGATG	GGTGTGGCTCCACTTTAACG
chr12:8988417-8993416	0	Genomic background	TCCCCCTCTGGTCTGGAA	GGAGCCCTAAGGGTAGATGGA
chr13:109764225-109769224	0	Genomic background	AGTGTGCGCTGCAAGGACAGA	GGAGGGCACGGAGGGTACTG
chr18:32574622-32579621	0	Genomic background	GGGTACGGAGGGTGAAATTGA	CTGGCACCAAGGCAGACACTT
chr14:53492709-53497708	0	Genomic background	GGTACTAGAAAGCATGCACCGACTA	ATCAGTTGGCAGCAGTTACA
chr21:42399887-42404886	0	Genomic background	CCCCACCGGCCACTTC	AGAACCGGAGGGTCCACTGT
chr1:1061300-1066299	0	Genomic background	CACCCGGGCCAGCAA	GCTTCATATTCCGTCTGAGA
chr20:6051971-6056970	0	Genomic background	CCCTCCTCCCCAACTGGAT	AGTACATTGAGACACACCCTTTCAC
chr16:265061-270060	0	Genomic background	TGGCTGCTGCAGAGTGTGA	GAAGTGAGCCATGAGCCATCA
chr19:372792-377791	0	Genomic background	GCCTCAGAGGGAAAGCTCAGA	TGTGTACCAAGCACTACGTGAAGA
chr11:454686-459685	0	Genomic background	GCAGCCGATCCTGACAAAG	TAGATTGCACGTGGATGTTCTG
chr19:38485608-38485721	0	Fernandez	GGCGAGTCTGGTCTTGAG	CGGGACAGGCCTGGTCT
chr12:67488596-67488646	0	Fernandez	ACTTTGGTCTGGGCTCTGA	CCACGAACCGCACAAAGG
chr1:231485604-231485663	0	Fernandez	CGAAGCCGGCGTTCC	CGCCTCGTTACAGCATGGT
chr11:9551756-9551840	0	Fernandez	GCCCTCCTTTTTCAAACC	GCTTCCCGCGACCGTTA
chr4:160001035-160001125	0	Fernandez	GAGAATTCCAATCACCAAGCAA	AGAGCACAAAGGCTGCAGGTA
chr6:143812894-143812974	0	Fernandez	CTGAAGGGAGTGGAGGAAAGGA	TGGTAGAGAGCAGTATGAAACAAGT
chr4:100207457-100207591	0	Fernandez	TCTGGCCACGTGACGGATAT	GGAGAGACTCCACTCCCAGAA
chr11:9550950-9551012	0	Fernandez	GAGCCGGGCCAATCG	GTTGCCACCACGAAACCC
chr11:77025560-77025700	0	Fernandez	GAAAAGTGCATGTCAAGGAAACAG	GGCCACGTGGAGGACTTT

chr4:160001487-160001570	0	Fernandez	GCTCATCTGAACGGACCTCTAAA	GGGCCCCAGGAAACTATATTG
chr1:25917877-25918071	0	Fernandez	AAAATCGAAAAAGGAGGCCCAA	TCTAAGGCACGGTCAGACCAA
chr12:10452907-10452973	0	Fernandez	GCAGTAAACCTGCAGGGAGAGA	TGTTTCCTGTGCACGTGAGTT
chr5:78107926-78108794	0	Fernandez	GTGTGCCAGGCATTGTTCTG	CCTCTCTGTGCCTCGGTTTT
chr6:33493370-33494369	1	Li	CGCTGGTACAGGAGAGTTGATCT	GCTGCCACCCAGGTAAGAAG
chr10:50416779-50417778	0	Li	TGTTTTAACGCACGGGCAAGA	GGCAGCGGAGACAGCTTC
chr4:121345268-121346267	1	Li	CTGTGCCGGGTGTGACACTA	TTCCCTCGGCCCAACTA
chr12:56167434-56168434	0	Li	GAGGCCGCTGAACTCAGAAG	CACTCACGAACAGTCTCATTTCG
chr10:94342408-94343407	0	Li	GCCGAGTCGGTGCTTAGTTCT	TGGCCGTGGCGTTGT
chr6:26291303-26292302	0	Li	GGCCCCTGCTCGAAAAC	TCTGATTGTTATTTGTCGTGAAG
chr3:44777589-44778588	0	Li	GGCTGCGCTTCCGAAGA	GTTTCTGGCCCGCTTCAAG
chr19:54860438-54861437	0	Li	CCC GT CAG CTG AG GCT TAG AG	GGTCTGTTACCCAAAGAATGATAAGT
chr7:45700627-45701626	0	Li	CCTCCCAGCTGAGCACTTGT	GAGGAGGGTAAACGGTTTGATT
chr10:71833464-71834463	0	Li	ACCAGGCTCACAAACACTTAGCT	GGCTGAGGAAGAGAGTGGCTTA
chr2:26378774-26379772	0	Li	TGGAGCACTGCCTGACTAAAAC	AATACGACCTTCGGCCATGT
chr18:46067887-46068885	0	Li	ACTTCCTCATAGATGCCGTAC	CAATTAGGTGCCGTATATGTC
chr12:12655399-12656398	0	Li	GGCACTTAGGAGCCAAACCT	GGCAGCTGTTTCCCTTTGC
chr20:32927411-32928410	0	Li	TTCACTCGACGGCGTCACT	CGAGGTTGGCAAGGACAGAA
chr6:26704470-26705469	0	Li	CCTAAAAAGCCGGCATCAAC	AGGACAGGCAGAACCGAGAAAAG
chr21:35281075-35281678	0	Cawley	CTCCCCACTGTGTGGTTCC	GGCGGACGAAGCGAGATT
chr21:35155920-35156160	0	Cawley	GCTGTTGGCTGCCCTCAT	TACACAGCCCAAATGCAT
chr21:31854206-31854429	0	Cawley	AGCCTCGAGCGAAACCTTTC	CCCAGCCTTGTGTAAATGG
chr21:36119095-36119640	0	Cawley	AAGCTTCTGGAGGTGTGAGA	TTGTCTTCTTGTCCCACATCAA
chr21:39476460-39476901	1	Cawley	AGCGTGTTCATCGGCTACTGA	GTTCACGGACACACCAATTCC
chr21:37366390-37366576	0	Cawley	GCACACGGAACACTCAGCAA	TGAAC TGTTGATTCTTCTCCCTATG
chr22:18319512-18319870	0	Cawley	CCTCACACGTGCATCTGCAT	GGTCTTACCTCTCCAGCACAGTAGA
chr22:21272073-21272334	0	Cawley	ACATGGCCACCCCTGACCAT	TGTGTCACCGCGGAATGA
chr22:22380642-22380959	0	Cawley	CGGCTCAGACAGCCTGGAT	TGGCTGTGTTGTCTGTGTTG
chr21:33786088-33786309	0	Cawley	GGAAGGCAAGGCTGTTCC	GCAGGTTTAAGCCTCATGTATCTG

chr21:42486195-42486591	1	Cawley	GAGGAGCGAGGGCCAAAC	ATCTTGGTGTCCCTGAGCTCAGT
chr21:32358698-32359018	0	Cawley	ACAGCTGTAGGTGCTGCAGAGA	CAGCGCCCTTCAGTGCAT
chr21:33539053-33540224	0	Cawley	CAGAAAGCTGCCTGGCTAGT	GTGCCAAGTGTCAAGCTGGTT
chr21:45860794-45860934	1	Cawley	AGCTGCCTCGTCCTGGATAA	GCAGCCTGTGGTGCATACG
chr21:32918958-32919348	0	Cawley	CCTCAGGCACCCAAGTGACT	AAAACCAGCCAAAACCTACAAGA

Supplemental Table ST4: Target Gene Function regulated by the 593 Myc binding loci and their TF motif occupancy

Gene Target	Cluster size	Cluster Location	Binding location	Motifs found in the binding clusters								Gene Function	Expression
				E box	E2F1	EGR	AP-2	Elk-1	SP1	MAZ			
CGI-30	3	chr1:101203369-101203910	5' (273)	E box	E2F1								Up
ATXN7L2	3	chr1:109738258-109739311	1st intron	E box	E2F1	EGR				MAZ			
TNFRSF1B	3	chr1:12161684-12162371	1st intron	E box								apoptosis	
TNR	3	chr1:172213151-172213691	1st intron	E box								cell adhesion	
PRKCZ	3	chr1:2012963-2013248	5' (977)	E box								signal transduction	
MYOM3	3	chr1:24166656-24169155	intron	E box			AP-2		SP1	MAZ			
FLJ12903	3	chr1:32975108-32980601	intron	E box	E2F1								Down
NSEP1	3	chr1:42817774-42818173	1st intron	E box	E2F1	EGR						regulation of transcription	Up
PPAP2B	3	chr1:56638426-56640300	3' (32201)	E box								lipid metabolism	
ZZZ3	3	chr1:77859876-77861148	1st intron	E box	E2F1	EGR	AP-2		SP1	MAZ			Up
COL24A1	3	chr1:86329554-86330238	intron	E box								cell adhesion	
HPSE2	3	chr10:100983674-100984370	1st intron	E box	E2F1								
MXI1	3	chr10:112022749-112023631	intron	E box								regulation of transcription	Up
	3	chr10:119450140-	intergenic	E box									

		119452766									
SFXN4	3	chr10:120914869-120915292	5' (0)	E box	E2F1	EGR		SP1		ion transport	Up
BMI1	3	chr10:22649935-22650606	5' (102)	E box	E2F1	EGR	AP-2		MAZ	regulation of transcription	
COMTD1	3	chr10:76665435-76666159	5' (42)	E box	E2F1			SP1		protein prenylation	Up
KCNMA1	3	chr10:79105207-79106832	5' (38721)	E box							
LDHA	3	chr11:18371314-18372534	5' (687)	E box						glycolysis	Up
MRGX1	3	chr11:18934937-18935991	5' (22400)	E box							
	3	chr11:28583834-28585929	intergenic	E box	E2F1			Elk-1	SP1	MAZ	
FLJ10774	3	chr11:34083412-34083857	5' (83)	E box							Up
BC040981	3	chr11:65357449-65358518	5' (276)	E box	E2F1						intracellular signaling cascade
ULK1	3	chr12:131073681-131074451	3' (317)	E box				Elk-1			signal transduction
CDK4	3	chr12:56431764-56432434	1st intron	E box	E2F1	EGR					cell cycle
HMGB1	3	chr13:29917696-29918274	3' (13956)	E box					MAZ	DNA repair	Up
HMGB1	3	chr13:29936036-29936793	1st intron	E box				SP1	MAZ	DNA repair	Up
AK124332	3	chr13:44887607-44890994	3' (26277)	E box	E2F1			SP1			Down
TBC1D4	4	chr13:74952804-74953543	1st intron	E box	E2F1	EGR		SP1		intracellular signaling cascade	Up
ABCC4	3	chr13:94751240-94752029	5' (0)	E box	E2F1	EGR	AP-2	SP1		transport	
MTA1	3	chr14:104957573-104958970	1st intron	E box		EGR	AP-2	SP1	MAZ	regulation of transcription	Up
LOC90668	3	chr14:23579840-23581078	5' (16051)	E box							
GPHN	3	chr14:66043657-66044157	5' (0)	E box	E2F1			Elk-1		Mo-molybdopterin cofactor biosynthesis	Up
AB040942	3	chr14:90899948-90900766	5' (50585)	E box					MAZ		Down
C14orf132	3	chr14:95628846-95629844	5' (0)	E box							
EVL	3	chr14:99561057-99561717	5' (40110)	E box						actin filament organization	Down

AL512723	3	chr15:19203958-19204659	5' (60315)	E box								
INO80	3	chr15:39194673-39195279	1st intron	E box	E2F1	EGR						
AK092120	3	chr15:68524094-68526459	5' (18839)	E box								
IGF1R	4	chr15:97010778-97011620	1st intron	E box	E2F1				MAZ	regulation of cell cycle	Up	
PRM1	3	chr16:11313718-11314882	5' (31431)	E box	E2F1	EGR		SP1	MAZ	chromosome organization and biogenesis		
GSPT1	3	chr16:11916365-11916879	1st intron	E box	E2F1		Elk-1			G1/S transition of mitotic cell cycle	Up	
RPS2	4	chr16:1954453-1955088	5' (3)	E box	E2F1		AP-2	SP1		protein biosynthesis		
	3	chr16:58966201-58966807	intergenic	E box								
HSD11B2	3	chr16:66021204-66022286	5' (522)	E box	E2F1					glucocorticoid biosynthesis	Up	
HAGHL	3	chr16:718452-719179	intron	E box	E2F1	EGR	AP-2	SP1	MAZ	Pyruvate metabolism	Up	
FA2H	3	chr16:73370851-73371845	5' (5426)	E box						metabolism	Down	
CDH13	3	chr16:81531914-81534501	intron	E box	E2F1					cell adhesion		
KIAA0513	3	chr16:83655196-83659314	1st intron	E box	E2F1						Down	
	4	chr16:84007015-84009330	intergenic	E box				SP1				
ABR	3	chr17:1033186-1033957	5' (3663)	E box						intracellular signaling cascade	Up	
NR1D1	4	chr17:35508576-35509205	1st intron	E box	E2F1			SP1	MAZ	regulation of transcription	Up	
WIRE	3	chr17:35680260-35683492	intron	E box	E2F1						Down	
PNPO	3	chr17:43373374-43374118	5' (198)	E box						pyridoxine biosynthesis	Up	
PELP1	3	chr17:4553578-4554435	5' (66)	E box	E2F1	EGR		SP1	MAZ		Up	
GEMIN4	4	chr17:601737-602216	1st intron	E box	E2F1			SP1	MAZ	ribosome biogenesis	Up	
SLC16A6	3	chr17:63798955-63799611	5' (356)	E box	E2F1	EGR	AP-2	SP1	MAZ	transport	Down	
WBP2	3	chr17:71352817-71353610	intron	E box					MAZ		Down	
RNF157	3	chr17:71689636-71690468	intron	E box						protein ubiquitination		

SEPT9	3	chr17:72912587-72913381	intron	E box								Down
GNAL	3	chr18:11773781-11775469	intron	E box							signal transduction	
ATP5D	3	chr19:1200043-1200957	3' (4740)	E box	E2F1	EGR	AP-2		SP1	MAZ	transport	Up
CRSP7	3	chr19:16558842-16559680	1st intron	E box	E2F1			Elk-1			regulation of transcription,	
MDS032	3	chr19:17186862-17187770	5' (81)	E box				Elk-1	SP1	MAZ	transport	
LOC115098	3	chr19:17904306-17904684	5' (2393)	E box					SP1			Up
KLF16	3	chr19:1814855-1815477	5' (889)	E box	E2F1	EGR	AP-2		SP1	MAZ	regulation of transcription	Up
CHST8	3	chr19:38963098-38965432	3' (7597)	E box						MAZ	carbohydrate metabolism	
LTBP4	3	chr19:45803021-45803380	intron	E box			AP-2		SP1	MAZ		
FOSB	3	chr19:50645284-50645854	5' (17556)	E box	E2F1						regulation of cell cycle	
RCN3	3	chr19:54728658-54728979	intron	E box					SP1	MAZ		
TUBB4	3	chr19:6457143-6458688	5' (5167)	E box						MAZ	microtubule-based process	
MCOLN1	3	chr19:7493492-7494443	1st intron	E box	E2F1						transport	
TFCP2L2	3	chr2:10034053-10037691	5' (7861)	E box	E2F1					MAZ		
TSN	3	chr2:122228793-122229471	5' (259)	E box	E2F1	EGR			SP1		DNA recombination	Up
AK096920	4	chr2:132858101-132862823	5' (79066)	E box		EGR				MAZ		
BC064534	3	chr2:15070960-15072948	5' (44406)	E box								
FLJ13984	3	chr2:172115248-172115708	1st intron	E box								Up
MGC35154/PT MA	3	chr2:232304945-232305474	3' (20589)	E box			AP-2					
LOC150678	3	chr2:240795552-240796717	5' (582)	E box	E2F1			Elk-1				
RNPEPL1	3	chr2:241239228-241239556	3' (1249)	E box							proteolysis and peptidolysis	
BCL11A	3	chr2:60690086-60690800	1st intron	E box	E2F1					MAZ	regulation of transcription	Down
MAD	3	chr2:70052823-70053574	5' (779)	E box	E2F1						regulation of transcription	

PCBP1	3	chr2:70224902-70225259	5' (1308)	E box	E2F1					mRNA metabolism	
PCBP1	3	chr2:70225524-70226104	5' (580)	E box	E2F1				SP1	MAZ	mRNA metabolism
AK131348	3	chr20:15779750-15781576	intron	E box							
NKX2-2	3	chr20:21471611-21476505	5' (32150)	E box				Elk-1		MAZ	regulation of transcription
BC036544	3	chr20:26209279-26213278	5' (73670)	E box							
ID1	3	chr20:29647185-29648223	5' (8801)	E box							regulation of transcription
AK127957	3	chr20:36496927-36497290	5' (0)	E box	E2F1						
CEPB	3	chr20:48290059-48292427	3' (48424)	E box						MAZ	regulation of transcription
AK056306	3	chr20:58523987-58529966	3' (70449)	E box			AP-2				
TIAM1	3	chr21:31382496-31388273	intron	E box	E2F1	EGR					signal transduction
KCNJ6	3	chr21:37994772-37995594	intron	E box							transport
FLJ45139	3	chr21:39155064-39156047	3' (15190)	E box							
WDR4	3	chr21:43171827-43172316	1st intron	E box	E2F1		AP-2				tRNA processing
C21orf33	3	chr21:44399780-44400522	3' (10211)	E box							
AY866799	3	chr21:9790802-9796383	5' (90018)	E box	E2F1				SP1	MAZ	
DGCR8	3	chr22:18455850-18456613	intron	E box							
HTF9C/RANBP1	7	chr22:18479043-18480456	5' (54)	E box	E2F1		AP-2	Elk-1	SP1		signal transduction
AK128501	3	chr22:21946828-21948619	5' (2568)	E box	E2F1						signal transduction
EWSR1	3	chr22:27988982-27989805	1st intron	E box	E2F1	EGR	AP-2		SP1	MAZ	regulation of transcription
PISD	3	chr22:30350977-30351708	1st intron	E box	E2F1	EGR			SP1		phospholipid biosynthesis
MFNG	3	chr22:36204556-36205864	1st intron	E box			AP-2	Elk-1	SP1	MAZ	development
KIAA0063	4	chr22:37420922-37423335	5' (582)	E box	E2F1	EGR	AP-2		SP1		
PIM3	3	chr22:48675342-48676938	intron	E box	E2F1	EGR	AP-2	Elk-1		MAZ	

BC017840	3	chr3:106565948-106566761	5' (2037)	E box								
AK130575	3	chr3:107246507-107246971	3' (27678)	E box								
PDIR	3	chr3:124268295-124269214	5' (0)	E box	E2F1		AP-2			electron transport	Up	
BC041080	3	chr3:127117990-127118654	5' (0)	E box	E2F1	EGR		SP1				
XRN1	3	chr3:143480998-143481733	3' (26634)	E box							Down	
MYL3	3	chr3:46874387-46874825	intron	E box						muscle development		
GNAI2	3	chr3:50243811-50247031	5' (3762)	E box	E2F1	EGR			MAZ	signal transduction	Down	
SH3BP2	3	chr4:2834278-2835028	5' (23006)	E box						signal transduction		
FLJ35424	3	chr4:3643501-3644275	3' (14399)	E box			Elk-1		MAZ			
PAICS	4	chr4:57143317-57143689	intron	E box						purine nucleotide biosynthesis	Up	
SRP72	3	chr4:57174516-57175257	1st intron	E box			Elk-1	SP1		protein targeting	Up	
TRIO	3	chr5:14270631-14271114	1st intron	E box						transmembrane receptor protein tyrosine phosphatase signaling pathway		
NPM1	4	chr5:170747835-170748452	1st intron	E box					MAZ	ribosome assembly	Up	
MXD3	4	chr5:176671494-176672106	5' (332)	E box	E2F1	EGR		SP1		regulation of transcription		
CLIC1	3	chr6:31806358-31812270	intron	E box	E2F1				MAZ	transport		
BRD2	4	chr6:33045270-33046164	1st intron	E box					MAZ	spermatogenesis		
FKBP5	3	chr6:35760539-35765490	intron	E box	E2F1	EGR		SP1		protein folding	Up	
TFEB	3	chr6:41783220-41783946	intron	E box	E2F1	EGR				regulation of transcription	Down	
SLC12A9	3	chr7:100094707-100095283	5' (112)	E box		EGR		SP1		transport		
MYO1G	5	chr7:44798312-44799588	5' (7364)	E box	E2F1		Elk-1	SP1			Down	
FLJ10099	3	chr7:65829688-65830564	5' (342)	E box	E2F1		AP-2					
PFTK1	3	chr7:89894708-89895548	5' (88252)	E box						protein amino acid phosphorylation	Down	
LOC157567	3	chr8:101518999-101519854	3' (82547)	E box								

EIF3S6	3	chr8:109329769-109330175	1st intron	E box		EGR				protein biosynthesis	Up
LOC113655	3	chr8:145704440-145705717	5' (436)	E box		EGR		Elk-1	SP1		Up
ELP3	3	chr8:28006196-28007083	5' (0)	E box					SP1	MAZ	ATP biosynthesis
TPD52	3	chr8:81269813-81274856	5' (25505)	E box							morphogenesis
G65583	3	chr9:10690721-10691643	3' (9949)	E box							
BC033399	3	chr9:119814256-119814992	3' (35051)	E box							
RPL35	3	chr9:124703050-124703729	1st intron	E box	E2F1					protein biosynthesis	
SET	3	chr9:128525031-128525413	5' (6136)	E box						DNA replication	Up
PPP2R4	4	chr9:128981268-128981871	intron	E box							
AK128680	3	chr9:130330712-130332309	5' (2648)	E box	E2F1					MAZ	
NOTCH1	3	chr9:136716631-136717573	5' (719)	E box				Elk-1		MAZ	regulation of transcription
SMARCA2	4	chr9:2147809-2148269	intron	E box							
OPRS1	3	chr9:34626888-34628157	intron	E box	E2F1				SP1		ergosterol biosynthesis
SHB	3	chr9:37989396-37990041	intron	E box							intracellular signaling cascade
RANBP6	3	chr9:5996835-5997428	3' (3963)	E box	E2F1	EGR	AP-2				transport
GLDC	3	chr9:6670386-6671904	5' (35725)	E box						MAZ	glycine metabolism
SECISBP2	3	chr9:89162638-89163295	5' (0)	E box		EGR		Elk-1	SP1		protein biosynthesis
ROR2	3	chr9:91566259-91567365	intron	E box				Elk-1			signal transduction
ANP32B	3	chr9:97826470-97827628	1st intron	E box	E2F1	EGR			SP1	MAZ	cell cycle
TRIM14	3	chr9:97960758-97961344	5' (0)	E box	E2F1	EGR			SP1		compartment specification
AK127862	3	chrX:112228272-112231634	intron	E box			AP-2				
DKC1	4	chrX:153554735-153555905	1st intron	E box	E2F1		AP-2	Elk-1	SP1		regulation of cell cycle
DKC1	3	chrX:153559303-153563698	intron	E box							regulation of cell cycle

UXT	3	chrX:47274140-47274567	1st intron	E box	E2F1				SP1		protein folding	
GPR173	4	chrX:52983477-52984760	1st intron	E box					SP1		signal transduction	
AB015434	3	chrX:58442141-58447986	3' (83430)	E box				Elk-1				
ITM2A	3	chrX:78370876-78371662	3' (50632)	E box								Up
AD-020	4	chr1:109354475-109355178	3' (3333)		E2F1							Down
KCNC4	3	chr1:110467590-110469114	1st intron									
KCNC4	3	chr1:110484580-110485210	3' (6329)						SP1	MAZ	transport	
KCND3	3	chr1:112229914-112230807	intron								transport	
ATP1A1	3	chr1:116635974-116636757	1st intron								metabolism	Up
CD2	3	chr1:116969524-116970172	5' (39295)								cell adhesion	Down
REG4	3	chr1:120098842-120099977	5' (33512)									
MGC57827	3	chr1:120550851-120551299	5' (427)									
AK095105	3	chr1:145701496-145701875	3' (55409)									
IFI16	3	chr1:155792567-155793804	5' (27)									
MPZ	3	chr1:158068428-158068816	3' (18882)						MAZ		cell adhesion	
AK094772	3	chr1:15906273-15907218	5' (0)		E2F1		AP-2		SP1	MAZ		
UCK2	3	chr1:162528440-162529144	5' (0)		E2F1	EGR	AP-2				biosynthesis	Up
CD3Z	3	chr1:164154151-164154692	1st intron								signal transduction	
PRRX1	3	chr1:167333122-167333987	5' (31656)								regulation of transcription	
GPR52	3	chr1:171193877-171194352	3' (44132)								signal transduction	
C1orf19	3	chr1:180850675-180851117	3' (75851)								mRNA processing	Up
CALML6	3	chr1:1878927-1879507	1st intron									
	3	chr1:211936077-211936784	intergenic									

USH2A	3	chr1:212648538-212649378	intron							electron transport	
CR749497	3	chr1:213452120-213452536	intron							regulation of transcription	
LOC128153	3	chr1:214424291-214425201	intron								
AK126238	3	chr1:218746309-218746730	3' (95527)								
FLJ10052	3	chr1:219811518-219812058	intron								
WNT4	3	chr1:22196736-22197965	intron						MAZ	frizzled-2 signaling pathway	
PARP1	3	chr1:222902186-222902949	5' (68)	E2F1		AP-2		SP1	MAZ	DNA repair	
ID3	3	chr1:23679624-23680503	5' (19231)						MAZ	regulation of transcription	
SMYD3	3	chr1:242526863-242528304	5' (82634)							chromatin modification	Up
RUNX3	3	chr1:25001229-25001807	5' (0)	E2F1					MAZ	regulation of transcription	
ZNF31	3	chr1:33611937-33612532	1st intron							regulation of transcription	
CSMD2	3	chr1:33978069-33979063	intron				Elk-1				
GRIK3	3	chr1:37117369-37118263	1st intron				Elk-1			transport	
M97016	3	chr1:39633570-39636018	intron						MAZ	cell differentiation	
MGC47816	3	chr1:42537593-42539876	intron	E2F1				SP1			
EIF2B3	3	chr1:44994681-44999066	intron	E2F1						protein synthesis	Up
SSBP3	3	chr1:54640352-54641437	5' (56949)							regulation of transcription	Down
DAB1	3	chr1:58326101-58327237	intron							cell differentiation	
JUN	3	chr1:59001216-59002100	5' (40181)							regulation of transcription	Down
SLC35D1	3	chr1:67267166-67267265	5' (35412)							transport	
	3	chr1:81058076-81058839	intergenic								
CYR61	3	chr1:85786662-85787567	3' (25907)							cell proliferation	
RPL5	3	chr1:93009380-93010106	1st intron	E2F1					MAZ	protein biosynthesis	Up

CPN1	3	chr10:101759381-101760204	3' (32412)		E2F1	EGR	AP-2		SP1		proteolysis and peptidolysis	
USMG5	3	chr10:105145912-105146785	5' (83)					Elk-1				Up
XPNPEP1	3	chr10:111672871-111673355	1st intron		E2F1	EGR	AP-2	Elk-1	SP1			
AK128746	3	chr10:38814364-38822801	3' (35822)		E2F1							
AK128746	4	chr10:38827281-38831512	3' (49528)									
AK128746	3	chr10:38832214-38840128	3' (55904)									
AK128746	4	chr10:38843294-38845836	3' (63901)				Elk-1					
AK128746	6	chr10:38853300-38858729	3' (76155)									
BC018500	3	chr10:39127317-39135251	intron		E2F1							
BC018500	3	chr10:39144365-39149661	intron									
AK131313	3	chr10:41981684-41986820	3' (90041)									
AK131313	3	chr10:42119885-42128729	1st intron									
CR749391	3	chr10:4582651-4583246	3' (28526)									
KIAA0514	3	chr10:46430138-46430689	3' (4669)									
BC033221	3	chr10:46516697-46517310	intron									
PRKG1	3	chr10:52483026-52483436	1st intron							signal transduction		
PRKG1	3	chr10:53102679-53103223	intron							signal transduction		
BC062346	3	chr10:5971799-5972239	5' (552)		E2F1		AP-2		SP1			Up
	3	chr10:62616603-62619388	intergenic									
LRRC20	3	chr10:71785240-71785746	intron									Up
CHST3	3	chr10:73379490-73380033	5' (14489)								carbohydrate metabolism	
MMRN2	3	chr10:88701762-88702404	1st intron							MAZ		
SBF2	3	chr11:10243018-10244300	1st intron									

CUL5	3	chr11:107431640-107437406	intron							cell cycle	
HYOU1	3	chr11:118432277-118433082	1st intron		E2F1	EGR			SP1	MAZ	glycolysis
AY358386	3	chr11:24789884-24790760	intron								
FLJ21924	3	chr11:32870349-32870917	5' (33298)				AP-2		SP1	MAZ	Up
M11S1	4	chr11:34030963-34031847	intron		E2F1			Elk-1	SP1	MAZ	Up
ELF5	3	chr11:34502806-34504376	5' (12179)								regulation of transcription
STIM1	3	chr11:3831757-3832981	5' (1355)						SP1	MAZ	cell cycle
	3	chr11:39059324-39060806	intergenic								
	3	chr11:48847007-48852861	intergenic		E2F1						
AX721283	3	chr11:56298617-56300346	5' (19829)								
RBM14	3	chr11:66140582-66141532	5' (0)		E2F1				SP1		DNA replication
ALDH3B1	3	chr11:67550758-67552459	intron			EGR			SP1		
TCIRG1	3	chr11:67561928-67563496	5' (857)						SP1	MAZ	hydrogen transport
AK125136	3	chr11:70673649-70674583	5' (0)								
RPLP2	4	chr11:799241-800260	5' (345)		E2F1	EGR	AP-2	Elk-1		MAZ	protein biosynthesis
DLG2	3	chr11:83149324-83150255	intron								
STK33	3	chr11:8493108-8494908	intron						SP1		protein amino acid phosphorylation
	3	chr11:90931599-90932281	intergenic								
ATP2A2	3	chr12:109181837-109183309	5' (0)		E2F1				SP1	MAZ	transport
ANAPC5	4	chr12:120252463-120253179	5' (7)							MAZ	cell cycle
BCL7A	3	chr12:120914651-120915314	5' (6689)								
KNTC1	3	chr12:121664939-121667575	3' (30323)							MAZ	cell cycle
PITPNM2	3	chr12:122160211-122160968	5' (284)	E box	E2F1		AP-2	Elk-1	SP1		

MPHOSPH9	3	chr12:122182908-122183789	intron							regulation of cell cycle	Up
MANSC1	3	chr12:12355121-12356133	3' (17913)		EGR						
BRI3BP	3	chr12:124002287-124003171	5' (137)	E2F1	EGR		SP1	MAZ			
	3	chr12:126476773-126477109	intergenic								
	4	chr12:130479494-130481135	intergenic					MAZ			
EP400	3	chr12:131138214-131138937	intron								
HIST4H4	3	chr12:14813796-14814531	3' (634)							chromosome organization and biogenesis	
KIAA0528	3	chr12:22587804-22588515	intron		AP-2					transport	
ETNK1	3	chr12:22823153-22823994	3' (93615)							phosphatidylethanolamine biosynthesis	Up
FLJ32894	3	chr12:24636217-24636725	5' (8193)								
MGC4266	3	chr12:3690549-3691114	intron								
NELL2	3	chr12:43189540-43190593	intron							cell adhesion	
LOC113251	3	chr12:49081031-49081814	1st intron	E2F1							Up
RARG	3	chr12:51899219-51899837	intron			Elk-1				regulation of transcription	
RPL41	3	chr12:54796669-54797483	1st intron							protein biosynthesis	
	3	chr12:89032043-89034220	intergenic								
AF429306	3	chr12:96519451-96520819	3' (59106)								
AK123478	3	chr13:113565099-113565484	3' (173)								Down
NUPL1	3	chr13:24770157-24770740	5' (3291)							transport	Up
13CDNA73	3	chr13:31554275-31555168	intron								Down
	3	chr13:33805449-33806415	intergenic								
LOC400120	3	chr13:36139574-36140250	5' (6038)								
KIAA1704	3	chr13:44464168-44464818	1st intron								Up

mir-17	3	chr13:90799144-90799791	5' (1068)				AP-2		SP1	MAZ		Up
EIF5	3	chr14:102873820-102875360	intron								protein biosynthesis	Up
BC033178	3	chr14:106257819-106258689	intron								immune response	
BC039714	3	chr14:21968215-21968773	intron								cellular defense response	
	3	chr14:31510282-31511260	intergenic									
ESR2	3	chr14:63794309-63794935	intron							MAZ	regulation of transcription	Down
BC044636	3	chr14:74296625-74297407	5' (3348)		E2F1							
C14orf159	3	chr14:90650293-90650920	5' (73)		E2F1				SP1			Down
BDKRB2	3	chr14:95698172-95698722	5' (42414)							MAZ	signal transduction	
C15orf2	3	chr15:22377164-22377879	5' (94507)							MAZ		
S82769	3	chr15:25026773-25027041	intron							MAZ		
HERC2	3	chr15:26198062-26199160	intron								ubiquitin cycle	Up
BAHD1	3	chr15:38520154-38520821	1st intron		E2F1		AP-2		SP1	MAZ		
GABPB2	3	chr15:48434697-48435455	5' (270)		E2F1						regulation of transcription	
SUHW4	3	chr15:54870749-54871574	5' (57972)									
RORA	3	chr15:58625091-58627069	intron					Elk-1			regulation of transcription	
RORA	3	chr15:58936935-58938114	1st intron								regulation of transcription	
SLC24A1	3	chr15:63706056-63706505	intron									
BX641106	3	chr15:69551549-69551986	intron									
AK124841	3	chr15:71882709-71884201	5' (65605)									
CYP11A1	3	chr15:72439801-72442600	1st intron								lipid metabolism	
ENC2??	3	chr15:84138539-84139341	5' (6)		E2F1				SP1	MAZ		
	3	chr15:86043835-86044582	intergenic									

SLCO3A1	3	chr15:90242181-90242899	1st intron							transport	
AK126539	3	chr16:11472339-11472704	intron								
ERCC4	3	chr16:13887785-13888258	5' (33529)							DNA repair	
AK126948	3	chr16:14143230-14143924	intron								
TMC5	4	chr16:19342144-19347258	5' (11943)	E2F1	EGR	Elk-1					
BC068999	3	chr16:21738704-21739586	5' (79)						MAZ	transcription from RNA polymerase I promoter	
RNPS1	3	chr16:2257677-2258525	5' (65)	E2F1			SP1			transcription	
NSMCE1	3	chr16:27150510-27151275	intron		EGR					intracellular signalling cascade	
LOC114984	3	chr16:2894586-2895419	3' (5631)	E2F1				MAZ			
BCL7C	3	chr16:30793484-30794896	3' (12355)	E2F1		AP-2	Elk-1				
AY587847	3	chr16:33779994-33789904	3' (84189)								
AY587847	3	chr16:33791143-33793606	3' (75600)								
AY587847	5	chr16:33799865-33807645	3' (65344)	E2F1							
AY587847	3	chr16:33870025-33870895	5' (325)	E2F1			SP1				
BC029861	3	chr16:34040151-34053555	5' (64996)								
	4	chr16:44944693-44950534	intergenic								
FLJ43980	4	chr16:44959775-44965005	3' (99397)								
FLJ43980	5	chr16:44974812-44980790	3' (83333)								
FLJ43980	5	chr16:44986539-45004644	3' (71665)								
FLJ43980	3	chr16:45004658-45011322	3' (56798)								
	3	chr16:57801983-57802713	intergenic					MAZ			
	3	chr16:57967439-57968972	intergenic								
CDH11	3	chr16:63766983-63767788	5' (54182)								

A2BP1	3	chr16:6664590-6666113	intron							mRNA processing	
AL833826	3	chr16:69713929-69714400	intron								
LOC124491	4	chr16:74056102-74056601	5' (232)		E2F1						
CDH13	3	chr16:81677434-81677714	intron							cell adhesion	
CDH13	3	chr16:82160443-82161072	intron							cell adhesion	
JPH3	3	chr16:86246285-86249007	intron								
FLJ45455	3	chr17:11383815-11386650	intron						MAZ		
DNAH9	3	chr17:11739500-11740142	intron							cell motility	
RPL23A	3	chr17:24070343-24071822	5' (201)		E2F1			Elk-1		protein biosynthesis	
TRAF4	3	chr17:24094598-24095541	5' (0)		E2F1	EGR	AP-2		SP1	MAZ	apoptosis
SSH2	3	chr17:25250538-25256234	1st intron							MAZ	protein amino acid dephosphorylation
CRLF3	3	chr17:26175714-26176264	5' (260)								Down
CRK7	3	chr17:34871225-34872507	5' (0)						SP1	MAZ	protein amino acid phosphorylation
U5-116KD	3	chr17:40331769-40332416	1st intron		E2F1						protein biosynthesis
SP2	3	chr17:43327123-43327391	5' (1416)								regulation of transcription
SLC25A11	3	chr17:4783431-4784220	5' (0)		E2F1		AP-2				transport
GDPD1	3	chr17:54759009-54759984	3' (52947)								glycerol metabolism
KCNH6	3	chr17:58961776-58963541	intron			EGR		Elk-1			transport
	3	chr17:60800980-60801805	intergenic								
PSMD12	3	chr17:62759670-62760373	3' (4405)								Up
BC034818	3	chr17:67590758-67592179	intron			EGR					
SLC16A11	3	chr17:6886902-6887537	1st intron		E2F1		AP-2		SP1		transport
FLJ20255	3	chr17:70311900-70313763	intron		E2F1						amino acid transport

DERP6	3	chr17:7096154-7096766	intron		E2F1		AP-2		SP1	MAZ		Up
AB058686	4	chr17:71108982-71110419	intron		E2F1					MAZ		
SIAT7B	3	chr17:72075719-72076467	intron								protein amino acid glycosylation	
raptor	3	chr17:76393827-76394680	intron									
ALOX15B	3	chr17:7886998-7887495	intron			EGR					lipid metabolism	
C18orf43	3	chr18:12410110-12410833	intron		E2F1	EGR	AP-2		SP1	MAZ		Up
ROCK1	4	chr18:16765024-16771741	3' (19547)								apoptosis	
ROCK1	7	chr18:16772104-16774327	3' (14573)								apoptosis	
C18orf45	3	chr18:19186616-19188046	intron		E2F1							
	3	chr18:26217340-26217834	intergenic									
KIAA1012	3	chr18:27769040-27774406	intron		E2F1						transport	Down
AK131454	3	chr18:29487996-29488965	intron									
AK090603	3	chr18:35709095-35709603	5' (75093)									
	3	chr18:39559962-39560661	intergenic									
HDHD2	3	chr18:42930249-42930956	1st intron		E2F1		AP-2	Elk-1	SP1		metabolism	
BCL2	3	chr18:58959991-58960414	intron							MAZ	apoptosis	Down
AK127618	3	chr18:74242147-74245211	1st intron									
USP14	10	chr18:96509-101573	5' (50229)							MAZ	ubiquitin-dependent protein catabolism	Up
	34	chr19:32423875-32435951	intergenic					Elk-1		MAZ		
	3	chr19:32648918-32654288	intergenic							MAZ		
AK098372	3	chr19:35403521-35405134	intron						SP1	MAZ		
LOC147991	3	chr19:37588236-37588868	5' (100)		E2F1	EGR		Elk-1	SP1	MAZ		
DPP9	3	chr19:4658995-4660623	intron								proteolysis and peptidolysis	

CEACAM5	3	chr19:46901501-46902795	5' (2184)		E2F1					cell adhesion	
EML2	3	chr19:50837141-50838148	5' (3345)		E2F1					visual perception	
ZNF541	4	chr19:52795036-52795733	5' (55061)		E2F1			SP1			
ARHGEF18	3	chr19:7308290-7308612	5' (43491)								
AY203939	3	chr19:7700750-7702714	intron		E2F1	EGR		SP1	MAZ		
FLJ46061	3	chr19:8313052-8315247	1st intron		E2F1	EGR	AP-2	SP1	MAZ		
NPAS2	3	chr2:101020021-101020700	intron							regulation of transcription	
AK126958	3	chr2:104657820-104658275	3' (62253)								
BUB1	3	chr2:111154334-111154495	5' (2540)							cell cycle	Up
POLR1B	3	chr2:113029725-113030524	intron							transcription	Up
BC057764	3	chr2:132831699-132840402	5' (83697)								
DKFZP566N034	3	chr2:135260733-135261370	intron								
NXPH2	3	chr2:139222467-139223153	3' (39503)							neuropeptide signaling pathway	
	3	chr2:145953505-145954212	intergenic								
	4	chr2:147602228-147602853	intergenic			EGR					
ORC4L	3	chr2:148610235-148610982	1st intron		E2F1					DNA replication	Up
	3	chr2:151814071-151819452	intergenic						MAZ		
DDX1	3	chr2:15682082-15682941	5' (0)				Elk-1		MAZ	ribosome biogenesis	Up
PLA2R1	3	chr2:160656649-160657351	intron								
BC037813	3	chr2:161543698-161544047	5' (11228)								
MTX2	3	chr2:177028879-177029745	3' (1206)							transport	Up
KCNS3	3	chr2:18033759-18034460	intron							transport	
MYO1B	3	chr2:192206407-192207125	3' (91375)							cytoskeleton organization and	Up

										biogenesis	
CD28	3	chr2:204438507-204439405	3' (13157)							immune response	
PUM2	3	chr2:20471578-20471991	5' (22962)		E2F1		AP-2		MAZ		
CPO	3	chr2:207684018-207685768	3' (25876)								
ZNF142	4	chr2:219349249-219350216	5' (0)		E2F1			SP1		regulation of transcription	
DKFZp547E052	3	chr2:227618221-227618882	intron								
ARL7	3	chr2:235196872-235199883	5' (12349)							signal transduction	Down
BC062988	3	chr2:42241113-42241543	3' (43943)			EGR			MAZ		
COX7A2L	3	chr2:42491543-42492369	intron						MAZ	electron transport	
MTA3	3	chr2:42728316-42729153	intron							regulation of transcription	Down
ACYP2	4	chr2:54254192-54254802	5' (0)				Elk-1		MAZ	phosphate metabolism	
AK056269	3	chr2:59321105-59321704	5' (35026)								
XPO1	3	chr2:61629310-61629543	intron							protein-nucleus import, docking	
BC044918	3	chr2:6501156-6501961	5' (35248)								
AK127187	4	chr2:69609904-69610347	5' (5123)								
EGR4	3	chr2:73423471-73423749	3' (6055)		E2F1					regulation of transcription	
CTNNA2	3	chr2:80748510-80748915	intron							cell adhesion	
SIAT9	3	chr2:86038381-86039231	5' (11174)					SP1		carbohydrate metabolism	Down
BX649136	3	chr2:91711687-91719076	3' (52721)		E2F1						
BC036700	3	chr20:12797304-12799455	intron		E2F1						
AK074473	3	chr20:13197295-13197576	5' (23571)						MAZ		
SNRPB2	3	chr20:16612695-16613644	5' (45416)							mRNA processing	Up
FOXA2	3	chr20:22590744-22592705	5' (79023)			EGR			MAZ	regulation of transcription	

BC018500	3	chr20:29278820-29284677	3' (13648)									
BC018500	3	chr20:29287621-29290975	3' (5312)		E2F1							
PDRG1	3	chr20:29999352-30004041	1st intron		E2F1		Elk-1	SP1				
RNPC2	3	chr20:33793360-33794031	5' (63)		E2F1					mRNA processing		Down
PTPRT	3	chr20:41127002-41127610	1st intron						MAZ	protein amino acid dephosphorylation		
AK131203	3	chr20:54564320-54570194	5' (30538)									
	3	chr21:23290985-23291584	intergenic									
BC040319	3	chr21:25279612-25279972	intron									
BC040319	3	chr21:25435027-25438308	5' (83931)									
KCNJ6	3	chr21:37889112-37889720	3' (29371)				SP1	MAZ		transport		
CRYAA	3	chr21:43484467-43485136	3' (19139)							protein folding		
ATP6V1E1	3	chr22:16464483-16465207	intron							transport		
TOP3B	3	chr22:20656410-20657356	1st intron		E2F1				MAZ	chromosome organization and biogenesis		
BC073770	3	chr22:21602207-21602729	3' (28933)				SP1			immune response		
AK126983	4	chr22:22580606-22581220	5' (6972)		E2F1	EGR		SP1				
BX647841	3	chr22:25565889-25566616	5' (12872)									
KIAA1043	3	chr22:26757271-26760612	intron			EGR						
NF2	3	chr22:28411702-28412574	intron						MAZ	cell cycle		Up
DEPDC5	3	chr22:30474085-30474488	5' (377)		E2F1			SP1		intracellular signalling cascade		Down
TIMP3	3	chr22:31431557-31432066	5' (90402)							transmembrane receptor protein tyrosine kinase signalling pathway		
TMPRSS6	3	chr22:35824046-35824573	5' (95)					SP1		proteolysis and peptidolysis		
LOC91689	3	chr22:40799408-40800424	5' (20)					SP1				

TOMM70A	3	chr3:101601866-101602899	5' (0)		E2F1			Elk-1				Up
	3	chr3:111724845-111725836	intergenic						SP1			
ZBTB20	3	chr3:115598665-115599186	intron							regulation of transcription		Down
SEC61A1	3	chr3:129253482-129254113	5' (5)		E2F1		AP-2		SP1	MAZ	transport	Up
RNF184	3	chr3:137397452-137397996	5' (1007)		E2F1	EGR			SP1	MAZ	protein ubiquitination	
AF424542	3	chr3:138360899-138361420	intron									
CHL1	3	chr3:140897-141375	5' (72439)							signal transduction		
G36586	3	chr3:151477043-151478167	5' (71274)									
ADMP	3	chr3:162519026-162519603	3' (25928)									
RAFTLIN	3	chr3:16478305-16479036	intron									Down
TBC1D5	3	chr3:17235678-17236271	intron									Down
PSARL	3	chr3:185085254-185085863	5' (63)		E2F1			Elk-1				Up
DNAJB11	3	chr3:187770954-187771673	5' (98)		E2F1					protein folding		Up
CPN2	3	chr3:195468051-195470735	3' (72653)		E2F1		AP-2			MAZ	protein stabilization	
BC064408	3	chr3:40848288-40849358	3' (70219)									
BC040739	3	chr3:41261243-41262635	3' (1239)									
PPP4R2	3	chr3:73099050-73099621	5' (29176)									Up
AF226994	3	chr3:75948365-75949082	5' (78376)									
GBE1	3	chr3:81849213-81849500	1st intron							carbohydrate metabolism		Up
IGSF4D	3	chr3:85666715-85667263	1st intron									
SEC24B	3	chr4:110742860-110743580	intron							transport		
FLJ20647	3	chr4:110857124-110857988	1st intron									
BC041920	3	chr4:127461081-127461743	3' (2280)									

FLJ10378	3	chr4:129452334-129453135	intron									Up
	3	chr4:145581561-145582075	intergenic									
LOC152485	3	chr4:147307686-147308556	5' (91058)									Down
AK057895	3	chr4:148411932-148412631	3' (96547)									
KIAA0922	3	chr4:154901504-154902016	intron				Elk-1		MAZ			Down
ADAM29	3	chr4:176345446-176346157	3' (71864)							proteolysis and peptidolysis		
BX640780	3	chr4:177751141-177751816	5' (96323)									
MLR1	3	chr4:17778686-17779574	5' (79523)									
CARF	3	chr4:184692451-184693405	5' (48004)							regulation of transcription	Up	
	3	chr4:22871102-22871764	intergenic									
FLJ21511	3	chr4:48993742-48998506	3' (91573)									
AK090412	3	chr4:49419971-49420804	5' (73437)									
AK098337	4	chr4:49474637-49482397	5' (15983)	E2F1								
AK098337	3	chr4:49483127-49488947	5' (25090)	E2F1								
AK098337	3	chr4:49492999-49499773	5' (31714)	E2F1								
CENPC1	3	chr4:68094350-68094812	3' (72283)									
GRPEL1	3	chr4:7275937-7276704	5' (88405)							protein folding	Up	
DKFZP564O082	3	chr4:76159365-76160107	5' (55753)							cell proliferation	Down	
G3BP2	3	chr4:76955235-76956430	5' (8)		EGR	AP-2		SP1			Up	
DKFZp686L181	3	chr4:84245778-84246754	intron				Elk-1					
MAPK10	3	chr4:87545360-87546384	intron							signal transduction		
MGC48628	3	chr4:92057988-92058270	intron									
EPB41L4A	3	chr5:111560991-111561804	intron									

PPIC	3	chr5:122408668-122409261	5' (8733)							signal transduction	
LOC133619	3	chr5:126880790-126882175	1st intron		E2F1			SP1			Up
	3	chr5:144676188-144676912	intergenic								
KIAA0555	3	chr5:147136492-147137076	1st intron								
PPARGC1B	3	chr5:149089791-149090385	5' (0)		E2F1	EGR	AP-2	SP1	MAZ		Up
GABRB2	3	chr5:160652279-160653077	3' (489)							transport	
BC011998	3	chr5:163666253-163666800	5' (47300)								
RANBP17	3	chr5:170198948-170199344	5' (22451)							transport	
RNF44	5	chr5:175895611-175896621	1st intron					SP1	MAZ	protein ubiquitination	Down
	3	chr5:24997495-24998241	intergenic								
BC036004	3	chr5:25368733-25369106	3' (11712)								
PDZK3	3	chr5:31688201-31688822	1st intron							cell adhesion	
AY245866	3	chr5:59653736-59656195	1st intron							signal transduction	
PIK3R1	3	chr5:67646362-67648420	3' (17316)					SP1	MAZ	intracellular signalling cascade	Down
	3	chr5:67760228-67760759	intergenic								
SLC30A5	3	chr5:68328248-68328774	5' (97154)							cation transport	Up
MRPS27	3	chr5:71651442-71652201	5' (37)					SP1	MAZ	protein synthesis	Up
AP3B1	3	chr5:77242335-77242786	3' (91255)								
LNPEP	3	chr5:96383366-96384856	intron		EGR			MAZ		proteolysis and peptidolysis	Down
	3	chr5:97884118-97884517	intergenic								
	3	chr6:138080166-138080886	intergenic								
ABT1	3	chr6:26723662-26724400	3' (16487)		E2F1					transcription	Up
RPS18	3	chr6:33347663-33348550	1st intron					Elk-1		protein biosynthesis	

C6orf69	3	chr6:36518587-36519162	5' (0)					SP1	MAZ	potassium ion transport	
FOXP4	3	chr6:41628094-41629163	1st intron						MAZ	regulation of transcription	Down
BX647715	3	chr6:44772015-44773474	5' (34441)		E2F1		Elk-1		MAZ		
FBXO9	3	chr6:53038051-53038763	5' (0)		E2F1	AP-2		SP1		protein ubiquitination	
KCNQ5	3	chr6:73388348-73388933	5' (0)		E2F1	EGR	AP-2	SP1		transport	
KIAA1117	3	chr6:83919472-83920370	intron								Down
TTC11	3	chr7:100481149-100481867	1st intron				Elk-1	SP1		apoptosis	
FLJ20485	3	chr7:104708600-104709037	intron							tRNA processing	Up
PIK3CG	3	chr7:106099111-106099627	5' (527)							G-protein coupled receptor protein signaling pathway	
	3	chr7:118189018-118189771	intergenic								
SEC8L1	3	chr7:132600755-132601426	intron			EGR				transport	Up
CNTNAP2	3	chr7:146145584-146146324	intron					SP1		cell adhesion	
	3	chr7:14767329-14768089	intergenic						MAZ		
INSIG1	3	chr7:154434478-154435247	5' (92445)					SP1	MAZ	metabolism	
EIF3S9	3	chr7:2167501-2168295	5' (0)		E2F1	AP-2		SP1		protein biosynthesis	Up
LFNG	3	chr7:2334513-2335359	intron					SP1	MAZ		
AB020702	3	chr7:36179965-36180633	5' (211)		E2F1	AP-2					
ANLN	3	chr7:36252061-36253434	intron							regulation of exit from mitosis	Up
JTV1	3	chr7:5821602-5822294	5' (32)		E2F1	AP-2	SP1			protein biosynthesis	Up
ZFD25	3	chr7:63555606-63560000	5' (14346)		E2F1			MAZ		regulation of transcription	
VKORC1L1	3	chr7:64763041-64767975	5' (15123)		E2F1					vitamin K metabolism	Up
GTF2I	3	chr7:73521168-73521981	1st intron							regulation of transcription	
GLCCI1	3	chr7:7895466-7895979	intron								Down

GNGT1	3	chr7:92901034-92902014	1st intron							signal transduction	
AK126705	3	chr8:107230822-107231265	3' (91785)								
MYC	4	chr8:128819877-128821548	intron		E2F1			SP1	MAZ	regulation of transcription	Up
	3	chr8:134980800-134981303	intergenic								
FLJ31164	3	chr8:143510803-143512429	5' (29491)					SP1	MAZ		
PYCRL	3	chr8:144762583-144763520	5' (510)		E2F1	EGR		SP1	MAZ	proline biosynthesis	
OPLAH	3	chr8:145187571-145188280	5' (991)				AP-2	SP1		transport	
RNF122	3	chr8:33550420-33552520	5' (7419)			AP-2				protein ubiquitination	Down
AK056395	3	chr8:37314500-37315553	5' (7414)								
RAB11FIP1	3	chr8:37863170-37863450	1st intron								
SFRP1	3	chr8:41268256-41269787	intron							Wnt receptor signaling pathway	
LOC115294	4	chr8:52828576-52829320	3' (63668)							protein modification	Down
RPS20	3	chr8:57149388-57149829	5' (0)		E2F1		AP-2			protein biosynthesis	Up
AL137390	3	chr8:63011627-63013105	3' (52188)								
BC037345	3	chr8:64795404-64795922	5' (48883)								
AK126705	3	chr8:77302644-77304413	5' (15366)								
	3	chr8:80356173-80356505	intergenic								
	3	chr8:84094719-84095243	intergenic								
PRG-3	3	chr9:100885792-100886165	1st intron								
	3	chr9:101753297-101753871	intergenic								
	3	chr9:101765458-101767687	intergenic								
	3	chr9:103770051-103771268	intergenic								
EPB41L4B	3	chr9:109110620-109111232	intron		E2F1				MAZ		

AKAP2	3	chr9:109889968-109890414	5' (353)						MAZ	protein localization	Down
ZNF483	3	chr9:111325432-111326205	5' (41353)		E2F1	EGR	AP-2		SP1		regulation of transcription
ASTN2	3	chr9:117270091-117270668	5' (13482)								Up
TLR4	3	chr9:117545848-117546522	5' (30)							signal transduction	Down
CR594083	3	chr9:119401333-119401754	5' (35668)								
DKFZP434C212	3	chr9:125203542-125204422	intron								Up
PBX3	3	chr9:125731307-125732039	5' (26014)		E2F1		AP-2			regulation of transcription	
FPGS	3	chr9:127649074-127650018	intron				AP-2			one-carbon compound metabolism	
AK130201	4	chr9:136236474-136236948	5' (3545)						SP1	MAZ	
NF1B	3	chr9:14170772-14171484	intron							transcription	
	3	chr9:24134390-24139390	intergenic								
DOCK8	3	chr9:272603-273039	1st intron								Down
KIAA0020	3	chr9:2822990-2823562	intron					Elk-1		mRNA metabolism	
DNAJA1	3	chr9:33014653-33015294	5' (255)		E2F1			Elk-1		protein folding	
B4GALT1	3	chr9:33132228-33132800	1st intron							carbohydrate metabolism	Down
MELK	3	chr9:36477890-36478564	5' (84604)						SP1	MAZ	protein amino acid phosphorylation
AK057054	3	chr9:38224347-38224917	3' (35424)							MAZ	
AK124122	3	chr9:44370035-44372529	intron					Elk-1			
C9orf26	3	chr9:6211888-6212423	1st intron								
UHRF2	3	chr9:6402845-6403500	5' (55)		E2F1	EGR			SP1		
AK024225	3	chr9:64475511-64481755	3' (39521)		E2F1						
AK024225	3	chr9:64498756-64505404	3' (18226)		E2F1						
G43521	3	chr9:67046244-67051946	3' (10536)								

TJP2	3	chr9:69133773-69134481	3' (34311)									Up
GDA	3	chr9:72128039-72128673	3' (31637)								nucleic acid metabolism	
C9orf41	3	chr9:74872104-74872966	5' (0)		E2F1	EGR		SP1				Up
	3	chr9:75531348-75531656	intergenic									
GNA14	3	chr9:77346497-77348030	intron						MAZ	signal transduction		
AK126070	3	chr9:81810842-81812537	3' (17377)				Elk-1					
UBQLN1	3	chr9:83552343-83553175	5' (102)		E2F1			SP1		protein modification		Up
	3	chr9:85081529-85082329	intergenic									
SPIN	3	chr9:88156198-88158193	5' (75879)		E2F1	EGR		SP1	MAZ	cell cycle		
SEMA4D	3	chr9:89282257-89282965	intron							cell adhesion		Down
SYK	3	chr9:90681065-90681456	1st intron							intracellular signalling cascade		Down
AUH	3	chr9:91206142-91207101	5' (3062)						MAZ	metabolism		
IARS	3	chr9:92052692-92053328	intron							protein biosynthesis		Up
BICD2	3	chr9:92606799-92607611	5' (709)		E2F1	EGR	AP-2	Elk-1	SP1		microtubule-based movement	Up
SUSD3	3	chr9:92894849-92896706	5' (4251)						SP1	MAZ		
C9orf10	3	chr9:93381296-93381706	intron					Elk-1				Up
let-7	3	chr9:94015722-94016098	5' (1695)									
CR749467	3	chr9:98649327-98650006	5' (11577)		E2F1		AP-2		SP1			Up
FLJ22679	3	chrX:109015699-109017599	5' (35798)									Down
SEPT6	3	chrX:118601433-118602239	1st intron		E2F1					cell cycle		Down
	3	chrX:17031243-17031677	intergenic									
	3	chrX:26609443-26610519	intergenic									
	3	chrX:30208760-30211316	intergenic		E2F1							

AK127711	3	chrX:39403456-39405037	3' (11028)									
	3	chrX:41708837-41709281	intergenic									
	3	chrX:45261135-45262026	intergenic							MAZ		
	3	chrX:6475222-6477226	intergenic		E2F1							
AK093687	3	chrX:70995176-70996031	5' (52338)									
PNPLA4	3	chrX:7662277-7662782	3' (13947)							lipid metabolism		
AK098372	3	chrX:99232386-99233295	5' (66629)									

Supplemental Table ST5: 668 Myc direct target genes and their associated binding clusters

Known Gene Target	PET Cluster Location	E box	E2F1 motif	Binding Location	Distance	Regulation
ABCD3	chr1:94619012-94619456			1st intron		Up
ABLIM1	chr10:116273692-116274078			1st intron		Up
ACACA	chr17:32751759-32752217			1st intron		Up
ACACA	chr17:32759292-32761645			1st intron		Up
ACAS2L	chr20:24985640-24986210	TRUE		1st intron		Down
ACAT1	chr11:107497313-107498125	TRUE	TRUE	1st intron		Up
ACBD6	chr1:177203041-177203720	TRUE	TRUE	5'	314	Up
ACE	chr17:58903326-58904648			5'	4126	Down
ACN9	chr7:96381325-96382544			5'	9506	Up
ACP1	chr2:254653-255353			1st intron		Up
ACTN1	chr14:68377620-68383332	TRUE	TRUE	3'	28478	Up
AD-003	chr9:129468055-129468694	TRUE	TRUE	1st intron		Up
AD-020	chr1:109354475-109355178		TRUE	3'	3333	Down
ADCK2	chr7:139794142-139794725			5'	31741	Up
ADCY3	chr2:25054702-25054910			5'	1151	Up
ADRBK2	chr22:24284545-24285141			5'	349	Down
ADSL	chr22:39068796-39069286			1st intron		Up
AGPS	chr2:178082849-178083607		TRUE	5'	0	Up
AK2	chr1:33170475-33170758			1st intron		Up
AK3	chr1:65358206-65359077	TRUE		1st intron		Up
AK3	chr1:65326152-65326573		TRUE	1st intron		Up
AKAP1	chr17:52517008-52517630		TRUE	5'	280	Up
AKAP11	chr13:41865754-41865967	TRUE		3'	70431	Down
AKAP13	chr15:83762475-83763079			1st intron		Down
ALOX5	chr10:45188990-45189652		TRUE	5'	487	Down
AMMECR1	chrX:109372811-109373731		TRUE	5'	5904	Up
AMN	chr14:102464629-102465090			intron		Up
ANAPC5	chr12:120252463-120253179			5'	7	Up
ANP32B	chr9:97826470-97827628	TRUE	TRUE	1st intron		Up
APBB1IP	chr10:26890977-26891431			intron		Down
APEH	chr3:49686655-49687079			5'	91	Up
APOL3	chr22:34786897-34787187	TRUE		3'	73893	Down
APP	chr21:26464177-26464530	TRUE	TRUE	1st intron		Up
APPBP1	chr16:65419837-65420498		TRUE	1st intron		Up
APPBP1	chr16:65421739-65422088		TRUE	1st intron		Up
APPBP1	chr16:65396104-65396653		TRUE	intron		Up
APRT	chr16:87405679-87406013		TRUE	5'	0	Up
ARHGAP6	chrX:11358808-11359409			1st intron		Up
ARHGEF11	chr1:153783941-153784462			1st intron		Down
ARHGEF7	chr13:110603871-110604771		TRUE	1st intron		Down
ARHGEF7	chr13:110612404-110613103			1st intron		Down
ARIH2	chr3:48931331-48931787		TRUE	5'	3705	Up
ARL5	chr2:152510398-152510989			5'	106	Up
ARL6IP6	chr2:153400908-153401383			1st intron		Up
ARL7	chr2:235196872-235199883			5'	12349	Down
ARPC1B	chr7:98623514-98623855	TRUE		1st intron		Down

ARPC5L	chr9:124713108-124713864			1st intron		Up
ARRDC3	chr5:90711853-90713048		TRUE	1st intron		Down
ASNS	chr7:97121683-97122471	TRUE		3'	4272	Up
ASNS	chr7:97144623-97145355			intron		Up
ASS	chr9:130355469-130356937			5'	409	Up
ATP1A1	chr1:116635974-116636757			1st intron		Up
ATP2A2	chr12:109181837-109183309	TRUE		5'	0	Up
ATP2A2	chr12:109183480-109184037			intron		Up
ATP2B4	chr1:200316970-200319478			5'	8630	Down
ATP5D	chr19:1200043-1200957	TRUE	TRUE	3'	4740	Up
ATP8A1	chr4:42498876-42499412			1st intron		Down
ATP8B1	chr18:53528639-53529433			1st intron		Down
AXUD1	chr3:39171034-39172440			5'	1775	Down
B3GNT1	chr2:62448432-62448778	TRUE		3'	84989	Down
B4GALT1	chr9:33132228-33132800			1st intron		Down
BACH	chr1:6259035-6259765			intron		Up
BAG1	chr9:33253231-33254074			1st intron		Up
BASP1	chr5:17285183-17285640			1st intron		Down
BCL2	chr18:58959991-58960414			intron		Down
BCL2A1	chr15:78050385-78051203			5'	104	Down
BCL3	chr19:49942816-49943487	TRUE	TRUE	5'	791	Down
BCLAF1	chr6:136652442-136653315		TRUE	5'	81	Up
BHLHB3	chr12:26154510-26155167		TRUE	3'	9392	Down
BHLHB3	chr12:26171406-26172232			5'	2725	Down
BICD2	chr9:92606799-92607611		TRUE	5'	709	Up
BICD2	chr9:92561534-92562098			intron		Up
BLK	chr8:11386722-11387084			5'	2080	Down
BMP7	chr20:55243421-55244057	TRUE		1st intron		Up
BNIP3	chr10:133687116-133690894	TRUE		5'	42365	Up
BNIP3L	chr8:26300587-26301031			1st intron		Down
BRDG1	chr4:68254533-68255039			1st intron		Down
BTBD5	chr14:44488216-44489260			1st intron		Down
BTG1	chr12:91042371-91042846		TRUE	5'	635	Down
BUB1	chr2:111154334-111154495			5'	2540	Up
BUB1B	chr15:38240561-38241074	TRUE		5'	0	Up
BUB3	chr10:124904027-124905075	TRUE	TRUE	intron		Up
C10orf119	chr10:121622283-121622791		TRUE	5'	64	Up
C11orf11	chr11:61208021-61208423			1st intron		Down
C13orf11	chr13:113260426-113260803			3'	8082	Down
C13orf25	chr13:90799144-90799791			1st intron		Up
C13orf3	chr13:20648075-20648725			1st intron		Up
C14orf104	chr14:49171199-49171842		TRUE	5'	1159	Up
C14orf159	chr14:90650293-90650920		TRUE	5'	73	Down
C14orf159	chr14:90745322-90751069	TRUE	TRUE	intron		Down
C14orf160	chr14:49848523-49849058		TRUE	5'	13	Up
C18orf24	chr18:46120942-46121407			5'	34183	Up
C18orf9	chr18:12692387-12693035		TRUE	5'	0	Up
C1orf19	chr1:180850675-180851117			3'	75851	Up
C1orf24	chr1:181638555-181638816			1st intron		Down
C1orf24	chr1:181678841-181679597		TRUE	5'	3855	Down
C1orf24	chr1:181506779-181509022	TRUE		intron		Down

C20orf27	chr20:3696132-3696650	TRUE		1st intron		Up
C21orf106	chr21:46702185-46702588			5'	1065	Down
C21orf5	chr21:36456241-36456557			5'	2266	Down
C22orf18	chr22:40666565-40667148	TRUE		intron		Up
C2F	chr12:6950201-6950535			5'	0	Up
C2orf3	chr2:75849249-75849505		TRUE	5'	0	Up
C5orf13	chr5:111144931-111145362	TRUE		5'	24289	Up
C6orf209	chr6:70563405-70564071			5'	260	Down
C6orf49	chr6:41856854-41857323			5'	0	Up
C6orf51	chr6:111359839-111363616	TRUE	TRUE	5'	23059	Up
C7orf24	chr7:30319839-30320440			5'	2590	Up
C8orf20	chr8:22054442-22055113			1st intron		Up
C9orf140	chr9:137238911-137239540			1st intron		Up
C9orf40	chr9:74796173-74797156	TRUE	TRUE	1st intron		Up
C9orf40	chr9:74798230-74798624			5'	1067	Up
C9orf41	chr9:74872104-74872966		TRUE	5'	0	Up
CABIN1	chr22:22876562-22876989		TRUE	1st intron		Down
CABIN1	chr22:22731694-22732463			5'	46	Down
CALM2	chr2:47314747-47315034			1st intron		Down
CALM2	chr2:47330561-47331846	TRUE		5'	16115	Down
CAMK1D	chr10:12581054-12581758			1st intron		Down
CAMK1D	chr10:12679336-12679788	TRUE		intron		Down
CAPG	chr2:85551272-85551947	TRUE		5'	2543	Down
CASP1	chr11:104411124-104413067			5'	215	Down
CBFA2T2	chr20:31543825-31544676			3'	2451	Down
CBFA2T3	chr16:87565775-87566236		TRUE	1st intron		Down
CBFA2T3	chr16:87572226-87572641			1st intron		Down
CBS	chr21:43356069-43359265	TRUE	TRUE	intron		Up
CBX6	chr22:37590983-37591995			intron		Up
CCM2	chr7:44813966-44814536		TRUE	1st intron		Down
CCNE2	chr8:95981252-95982982			5'	4844	Up
CCNJ	chr10:97792759-97793517		TRUE	5'	52	Up
CCT5	chr5:10313098-10314115	TRUE		intron		Up
CD44	chr11:35121915-35122880			1st intron		Down
CD47	chr3:109205531-109206038	TRUE		3'	39068	Down
CD97	chr19:14376477-14377023			intron		Down
CDC6	chr17:35697587-35698003		TRUE	5'	0	Up
CDCA7	chr2:174045512-174045837		TRUE	1st intron		Up
CDK4	chr12:56431764-56432434	TRUE	TRUE	1st intron		Up
CDKN2D	chr19:10538725-10539530			intron		Down
CEPB	chr20:48290059-48292427	TRUE		3'	48424	Up
CGI-30	chr1:101203369-101203910	TRUE	TRUE	5'	273	Up
CKS1B	chr1:151763862-151764375			intron		Up
CLN6	chr15:66309405-66309729	TRUE		5'	485	Up
CLN6	chr15:66345887-66346801			5'	9938	Up
COCH	chr14:30414163-30415075	TRUE	TRUE	intron		Up
COL9A2	chr1:40450068-40450805		TRUE	intron		Down
COMTD1	chr10:76665435-76666159	TRUE	TRUE	5'	42	Up
COPEB	chr10:3876716-3877191			5'	59597	Down
CORO2A	chr9:98012006-98014904			1st intron		Down
COX4I2	chr20:29677453-29679995	TRUE	TRUE	5'	10520	Down

	CRK7	chr17:34871225-34872507			5'	0	Up
	CRR9	chr5:1399243-1399508			5'	1408	Up
	CSDA	chr12:10766309-10766825	TRUE		1st intron		Up
	CSE1L	chr20:47104565-47104904			1st intron		Up
	CSRP2BP	chr20:18120816-18125818	TRUE	TRUE	3'	5940	Up
	CTDSPL	chr3:37880007-37880913			intron		Up
	CTPS	chr1:41114671-41115000		TRUE	1st intron		Up
	CTSB	chr8:11779521-11780148	TRUE		5'	16968	Down
	CTSB	chr8:11748124-11748420	TRUE		intron		Down
	CTSC	chr11:87710342-87710794		TRUE	5'	3	Up
	CXorf15	chrX:16564457-16565081	TRUE	TRUE	1st intron		Up
	CYCS	chr7:24938112-24938642		TRUE	5'	214	Up
	D21S2056E	chr21:44048490-44049598		TRUE	3'	0	Up
	D8S2298E	chr8:30721128-30721976	TRUE		1st intron		Up
	DAPK2	chr15:62015742-62021561	TRUE	TRUE	intron		Down
	DDX1	chr2:15682082-15682941			5'	0	Up
	DDX31	chr9:132574547-132575481	TRUE	TRUE	5'	0	Up
	DDX51	chr12:131294761-131295221		TRUE	5'	27	Up
	DEPDC5	chr22:30474085-30474488		TRUE	5'	377	Down
	DEPDC5	chr22:30485119-30492224	TRUE		intron		Down
	DERP6	chr17:7096154-7096766		TRUE	intron		Up
	DGCR6	chr22:17266087-17266623			5'	2022	Up
	DHODH	chr16:70599693-70600257	TRUE	TRUE	5'	105	Up
	DHX15	chr4:24148908-24149860		TRUE	3'	55727	Up
	DHX30	chr3:47857612-47858374			intron		Up
	DHX37	chr12:123998307-123998914	TRUE	TRUE	5'	2	Up
	DKC1	chrX:153554735-153555905	TRUE	TRUE	1st intron		Up
	DKC1	chrX:153559303-153563698	TRUE		intron		Up
	DKFZP564O0463	chr8:104496835-104497966			1st intron		Up
	DKFZP586L0724	chr17:63170413-63170922	TRUE		3'	0	Up
	DNAJA3	chr16:4412424-4415322		TRUE	5'	2364	Up
	DNAJB6	chr7:156629154-156629837		TRUE	1st intron		Up
	DNAJC12	chr10:69265648-69266062			1st intron		Up
	DNMT3B	chr20:30813418-30814088		TRUE	5'	68	Up
	DOCK10	chr2:225704957-225705481			1st intron		Down
	DOCK11	chrX:117444992-117449082		TRUE	1st intron		Down
	DOCK8	chr9:272603-273039			1st intron		Down
	DPH2L2	chr1:44104435-44104992	TRUE	TRUE	5'	0	Up
	DSCR2	chr21:39456398-39460284	TRUE		3'	10767	Up
	DSG2	chr18:27397876-27400764	TRUE	TRUE	3'	17952	Up
	DVL1	chr1:1317880-1320124			1st intron		Up
	E2IG2	chr11:73265269-73265859			5'	74	Up
	EHD1	chr11:64399133-64399718			1st intron		Down
	EIF2B3	chr1:44994681-44999066		TRUE	intron		Up
	EIF3S1	chr15:42621703-42622094			intron		Up
	EIF3S6	chr8:109329769-109330175	TRUE		1st intron		Up
	EIF3S6	chr8:109337386-109337755			5'	7520	Up
	EIF3S9	chr7:2167501-2168295		TRUE	5'	0	Up
	Ells1	chr7:29952210-29952477			1st intron		Up
	ENO1	chr1:8872342-8872815	TRUE		intron		Up
	ENTPD1	chr10:97587680-97588313	TRUE		intron		Down

EPS15	chr1:51666956-51667548	TRUE		1st intron	Down	
EPS15	chr1:51695877-51696824	TRUE		1st intron	Down	
ERBB2IP	chr5:65309652-65310059			1st intron	Down	
ERBP	chr1:94051714-94052317			intron	Up	
ESR2	chr14:63794309-63794935			intron	Down	
ETV6	chr12:11772562-11773584			1st intron	Down	
EVI2A	chr17:26672557-26673108			5'	172	Down
EVL	chr14:99561057-99561717	TRUE		5'	40110	Down
EXO1	chr1:238338582-238339174		TRUE	1st intron	Up	
EXOSC5	chr19:46595028-46595286	TRUE	TRUE	5'	27	Up
EXOSC7	chr3:44992824-44993696			1st intron	Up	
FA2H	chr16:73370851-73371845	TRUE		5'	5426	Down
FAH	chr15:78242116-78242715	TRUE		intron	Up	
FAH	chr15:78258521-78259290	TRUE		intron	Up	
FAIM	chr3:139810967-139811817			1st intron	Up	
FAM29A	chr9:19092801-19093187			5'	41	Up
FBS1	chr16:30578925-30582706		TRUE	5'	2830	Down
FBXL6	chr8:145547307-145547856			3'	2300	Up
FBXO10	chr9:37565980-37566699		TRUE	1st intron	Down	
FBXO31	chr16:85955184-85956036		TRUE	1st intron	Up	
FBXO31	chr16:85946986-85951415			1st intron	Up	
FCGR2A	chr1:158304096-158305126	TRUE		3'	1793	Down
FGD2	chr6:37082282-37082939			1st intron	Down	
FGD2	chr6:37126825-37127506	TRUE		3'	22412	Down
FGFR1	chr8:38441807-38442967			1st intron	Down	
FKBP11	chr12:47604581-47605144	TRUE		intron	Up	
FKSG14	chr5:64834784-64835548	TRUE		3'	14234	Up
FLJ00012	chr11:72211285-72211603	TRUE		intron	Down	
FLJ00332	chr11:66933099-66933499			intron	Down	
FLJ10330	chr1:108938957-108939321			5'	7874	Up
FLJ10378	chr4:129452334-129453135			intron	Up	
FLJ10407	chr1:54013369-54013798			1st intron	Up	
FLJ10504	chr1:152392527-152393251	TRUE	TRUE	5'	208	Up
FLJ10514	chr1:170550718-170556138	TRUE		intron	Up	
FLJ10569	chr8:19719309-19720439			intron	Up	
FLJ10774	chr11:34083412-34083857	TRUE		5'	83	Up
FLJ11088	chr12:28341689-28342160			1st intron	Down	
FLJ11286	chr19:10063449-10063933	TRUE		intron	Down	
FLJ12439	chr1:52875166-52875968	TRUE		1st intron	Up	
FLJ12519	chr2:190131827-190132226			1st intron	Up	
FLJ12903	chr1:32975108-32980601	TRUE	TRUE	intron	Down	
FLJ13089	chr12:111008606-111009562	TRUE	TRUE	5'	51	Up
FLJ13220	chr4:44521532-44521960		TRUE	5'	0	Up
FLJ13955	chr8:99417576-99419467	TRUE		5'	42635	Down
FLJ13984	chr2:172115248-172115708	TRUE		1st intron	Up	
FLJ14075	chr2:10780197-10780794			1st intron	Up	
FLJ14827	chr12:112088538-112089314			intron	Up	
FLJ20232	chr22:38223013-38223458			1st intron	Up	
FLJ20485	chr7:104708600-104709037			intron	Up	
FLJ21839	chr2:27185835-27186393			5'	30	Up
FLJ21924	chr11:32870349-32870917			5'	33298	Up

FLJ22104	chr11:86807901-86809713	TRUE		3'	96468	Up
FLJ22471	chr12:122969095-122969496			1st intron		Down
FLJ22679	chrX:109015699-109017599			5'	35798	Down
FLJ23441	chr11:77963329-77963564	TRUE		5'	87	Up
FLJ25476	chr1:33394467-33396386			5'	9851	Down
FLJ31434	chr1:37928493-37929361		TRUE	5'	1276	Up
FLJ31818	chr7:112168015-112169021		TRUE	1st intron		Down
FLJ31818	chr7:112116264-112116732	TRUE		intron		Down
FLJ32549	chr12:62902061-62902592	TRUE	TRUE	5'	0	Up
FLJ38482	chr4:166486609-166487125			1st intron		Up
FLJ39370	chr4:113435143-113435697			1st intron		Up
FNBP1	chr9:129866079-129866523			1st intron		Down
FNBP1	chr9:129877446-129878801			1st intron		Down
FOXP4	chr6:41628094-41629163			1st intron		Down
FREQ	chr9:130102222-130103623	TRUE	TRUE	3'	24342	Up
FSTL3	chr19:627521-629775	TRUE	TRUE	intron		Down
GAJ	chr4:154745331-154745945		TRUE	3'	51963	Up
GALNT2	chr1:226608681-226609350	TRUE		1st intron		Up
GALNT2	chr1:226563159-226564608			1st intron		Up
GBGT1	chr9:133065670-133066209			intron		Down
GCN1L1	chr12:119095199-119095498			5'	98	Up
GCSH	chr16:79686682-79687650	TRUE	TRUE	1st intron		Up
GEMIN4	chr17:601737-602216	TRUE	TRUE	1st intron		Up
GEMIN5	chr5:154297124-154297548	TRUE		1st intron		Up
GGH	chr8:64113283-64113912			1st intron		Up
GLCCI1	chr7:7895466-7895979			intron		Down
GLDC	chr9:6670386-6671904	TRUE		5'	35725	Up
GLRX2	chr1:189805608-189806577	TRUE	TRUE	5'	0	Up
GLUD1	chr10:88844118-88844865		TRUE	5'	0	Up
GNAS	chr20:56898335-56899042		TRUE	5'	892	Down
GNG10	chr9:111473091-111473743	TRUE	TRUE	5'	0	Up
GNG2	chr14:51440289-51440852			1st intron		Down
GOLPH2	chr9:85943251-85943700			1st intron		Up
GOLPH4	chr3:169296461-169296866	TRUE		5'	993	Up
GPHN	chr14:66043657-66044157	TRUE	TRUE	5'	0	Up
GPR125	chr4:22193264-22193615			1st intron		Up
GRPEL1	chr4:7275937-7276704			5'	88405	Up
GRPEL1	chr4:7188008-7188808			5'	653	Up
GRPEL2	chr5:148705287-148705612			1st intron		Up
GSPT1	chr16:11916365-11916879	TRUE	TRUE	1st intron		Up
GTF3A	chr13:26896850-26897207		TRUE	5'	0	Up
H6PD	chr1:9237774-9238280			1st intron		Down
HCK	chr20:30121907-30123117	TRUE		1st intron		Down
HCST	chr19:41086539-41086772		TRUE	intron		Down
HDLBP	chr2:241896702-241897385			intron		Up
HERPUD1	chr16:55522640-55523170	TRUE		5'	757	Down
HIC2	chr22:20124118-20124627			3'	0	Up
HIP1	chr7:75013455-75013893		TRUE	5'	779	Down
HIP2	chr4:39521877-39522338		TRUE	5'	330	Up
HLA-E	chr6:30568041-30568837			3'	288	Down
HMGA1	chr6:34313354-34314032		TRUE	1st intron		Up

HMGB1	chr13:29936036-29936793	TRUE		1st intron		Up
HMGB1	chr13:29917696-29918274	TRUE		3'	13956	Up
HMGB1	chr13:29880259-29880828		TRUE	3'	51442	Up
HMGCR	chr5:74666626-74667835			5'	1820	Up
HN1	chr17:70666719-70667778			5'	5033	Up
HNRPA3	chr2:177902020-177902936	TRUE		5'	361	Up
HNRPB	chr5:177563776-177564180	TRUE		5'	127	Up
HNRPF	chr10:43224174-43224634			5'	12393	Up
HNRPR	chr1:23416349-23416959	TRUE		5'	550	Up
HNRPU	chr1:241352807-241353302	TRUE		5'	0	Up
HS2ST1	chr1:87093053-87093595			1st intron		Up
HS2ST1	chr1:87291108-87292302	TRUE		3'	4180	Up
HSPA5	chr9:125099882-125100295			5'	16870	Up
HT008	chr17:59696222-59696559			5'	1982	Up
IARS	chr9:92052692-92053328			intron		Up
ICAM1	chr19:10240949-10241358	TRUE		5'	1568	Down
IDH3B	chr20:2587485-2588211			intron		Up
IER2	chr19:13123860-13124298	TRUE	TRUE	1st intron		Down
IFITM2	chr11:295657-297355			5'	2113	Down
IFRD2	chr3:50304275-50304736	TRUE	TRUE	intron		Up
IL17D	chr13:20176013-20176548		TRUE	intron		Up
IL4R	chr16:27282255-27283079	TRUE		3'	0	Down
IMMP2L	chr7:110795740-110796283	TRUE	TRUE	5'	0	Up
IMPDH1	chr7:127638195-127638734		TRUE	intron		Up
IPO7	chr11:9362707-9363612		TRUE	1st intron		Up
IRF2	chr4:185771019-185771440	TRUE		5'	45891	Down
IRF5	chr7:128167285-128167708	TRUE		5'	4504	Down
ISYNA1	chr19:18407350-18408941	TRUE	TRUE	intron		Up
ITGA4	chr2:182147514-182148139		TRUE	5'	0	Down
ITPKB	chr1:223138231-223138636		TRUE	intron		Down
ITPR2	chr12:26492972-26495411	TRUE		intron		Down
JTV1	chr7:5821602-5822294		TRUE	5'	32	Up
JUN	chr1:59001216-59002100			5'	40181	Down
KARS	chr16:74238731-74239131			1st intron		Up
KCMF1	chr2:85109407-85109909		TRUE	5'	578	Up
KCNN3	chr1:151631829-151632239			1st intron		Down
KCNN3	chr1:151650303-151650708			1st intron		Down
KIAA0082	chr6:37527415-37528179	TRUE		intron		Down
KIAA0090	chr1:19319823-19320430			1st intron		Up
KIAA0179	chr21:43907723-43910489	TRUE		1st intron		Up
KIAA0179	chr21:43903941-43904316	TRUE	TRUE	5'	0	Up
KIAA0247	chr14:69253672-69255556	TRUE		3'	3574	Down
KIAA0276	chr4:52567141-52568189			1st intron		Up
KIAA0355	chr19:39483186-39483707			5'	0	Down
KIAA0513	chr16:83655196-83659314	TRUE	TRUE	1st intron		Down
KIAA0831	chr14:54948254-54948499	TRUE		5'	93	Down
KIAA1117	chr6:83919472-83920370			intron		Down
KIAA1229	chr1:86576498-86576919			5'	2702	Down
KIAA1434	chr20:5534106-5534471			1st intron		Down
KIAA1536	chr12:52374760-52376133		TRUE	3'	15339	Down
KIAA1536	chr12:52415519-52415815			5'	8144	Down

KIAA1539	chr9:35106242-35107114	TRUE	5'	825	Down
KIF9	chr3:47294554-47295042		1st intron		Up
KLHL14	chr18:28613477-28613781		5'	6601	Down
KPNA4	chr3:161757286-161757754		1st intron		Up
LAPTM5	chr1:30899349-30899951		5'	54	Down
LARP	chr5:154114909-154115719	TRUE	intron		Up
LARP	chr5:154116605-154117309	TRUE	intron		Up
LASP1	chr17:34331018-34331350	TRUE	3'	0	Down
LASS2	chr1:147759487-147759895	TRUE	1st intron		Up
LAT1-3TM	chr16:29532398-29533034	TRUE	TRUE	5'	125
LDHA	chr11:18371314-18372534	TRUE		5'	Up
LDHA	chr11:18372584-18372792	TRUE	TRUE	5'	25
LEF1	chr4:109447494-109447855		TRUE	5'	Up
LILRB4	chr19:59856110-59856553			5'	9830
LNPEP	chr5:96383366-96384856			intron	Down
LOC113655	chr8:145704440-145705717	TRUE		5'	Up
LOC115098	chr19:17904306-17904684	TRUE		5'	Up
LOC115294	chr8:52828576-52829320			3'	63668
LOC122618	chr14:104421477-104423288			5'	Down
LOC123169	chr15:50053643-50057604		TRUE	5'	Up
LOC129285	chr2:48580006-48580628			1st intron	Down
LOC152485	chr4:147307686-147308556			5'	Down
LOC152485	chr4:147186850-147187687			1st intron	Down
LOC152485	chr4:147193331-147195035			1st intron	Down
LOC201164	chr17:17050379-17050914	TRUE	TRUE	5'	Up
LOC338692	chr11:66812342-66812674		TRUE	5'	Down
LOC348094	chr15:62980363-62980763			5'	Down
LOC56902	chr2:68296401-68296984	TRUE		5'	Up
LOC57168	chr22:25142931-25147018			5'	Down
LOC63929	chr22:39643549-39648224	TRUE		3'	Up
LOC64744	chr1:40509089-40509858			1st intron	Down
LOC64744	chr16:87279501-87280110			1st intron	Down
LOC85865	chr7:89624017-89624962			5'	Up
LOC90624	chr5:130540999-130541923			1st intron	Up
LPHN1	chr19:14190109-14191959	TRUE		5'	Up
LPHN1	chr19:14236840-14240962		TRUE	5'	Up
LSM11	chr5:157103097-157103615		TRUE	5'	Up
LSS	chr21:46473248-46473823		TRUE	5'	Up
LSS	chr21:46452391-46453838	TRUE		intron	Up
LSS	chr21:46466796-46467205	TRUE		intron	Up
LTA4H	chr12:94894723-94895755		TRUE	3'	Up
LY96	chr8:75063315-75065247			5'	Down
M11S1	chr11:34030963-34031847		TRUE	intron	Up
MAP3K8	chr10:30742323-30743360	TRUE		5'	Down
MAPK1	chr22:20551353-20552062			5'	Down
MATK	chr19:3736637-3737332	TRUE	TRUE	1st intron	Up
MAZ	chr16:29725212-29726225		TRUE	intron	Up
MBNL1	chr3:153511458-153512020			1st intron	Up
MBNL1	chr3:153533000-153533459			1st intron	Up
MCM3	chr6:52228684-52230942	TRUE		3'	Up
MCM3	chr6:52257170-52257888		TRUE	5'	Up

MCM4	chr8:49035675-49035894		TRUE	5'	303	Up
METAP1	chr4:100274279-100274828		TRUE	1st intron		Up
MFNG	chr22:36204556-36205864	TRUE		1st intron		Up
MGAT4A	chr2:98803102-98804048			5'	2219	Down
MGC13017	chr5:133800638-133801221	TRUE		5'	25518	Up
MGC13170	chr19:55999781-56000386		TRUE	5'	5673	Up
MGC14151	chr17:7701641-7702328	TRUE	TRUE	5'	0	Up
MGC14798	chr15:33625441-33626142			5'	167	Up
MGC15763	chr3:16281552-16281943			5'	0	Up
MGC23909	chr5:82405033-82405321			1st intron		Up
MGC2603	chr1:25869927-25870184	TRUE		5'	10	Up
MGC27085	chr3:171012343-171012916		TRUE	1st intron		Up
MGC3207	chr19:13736292-13736644			5'	0	Up
MGC45866	chr15:87919143-87920054		TRUE	5'	31658	Up
MGC5306	chr11:93113492-93114474	TRUE	TRUE	5'	0	Up
MGC8407	chr3:49883727-49885425	TRUE	TRUE	5'	1744	Up
MGEA5	chr10:103567917-103568573			5'	81	Down
MGST2	chr4:140940258-140940656			5'	4187	Up
MINA	chr3:99173165-99173681	TRUE		5'	0	Up
MLLT3	chr9:20620700-20621050			5'	8345	Down
MLSTD1	chr12:29193470-29193932		TRUE	1st intron		Up
MLSTD1	chr12:29131121-29131501	TRUE		5'	62048	Up
MOBKL2B	chr9:27478055-27478769			1st intron		Down
MPP6	chr7:24386523-24387122		TRUE	1st intron		Up
MPP6	chr7:24384653-24385012			5'	1494	Up
MPP6	chr7:24317222-24317754	TRUE		5'	68857	Up
MRPL1	chr4:79141084-79141428			1st intron		Up
MRPL21	chr11:68424494-68424822			intron		Up
MRPL23	chr11:1951951-1952259			3'	17739	Up
MRPL32	chr7:42745056-42745474		TRUE	5'	0	Up
MRPL37	chr1:54379240-54380481			1st intron		Up
MRPL39	chr21:25909336-25914379	TRUE		5'	11437	Up
MRPL48	chr11:73169666-73170286			5'	6064	Up
MRPS18B	chr6:30692993-30693573		TRUE	5'	280	Up
MRPS27/PTCD2	chr5:71651442-71652201			5'	37	Up
MRPS28	chr8:80966372-80968542			3'	26205	Up
MRPS7	chr17:70773185-70773524			3'	0	Up
MSF	chr17:72912587-72913381	TRUE		intron		Down
MSH2	chr2:47542468-47542818			1st intron		Up
MSL3L1	chrX:11535309-11535823	TRUE		5'	509	Down
MTAP	chr9:21793373-21794191		TRUE	1st intron		Up
MTAP	chr9:21786466-21786954			5'	5749	Up
MTAP	chr9:21729703-21730207	TRUE		5'	62764	Up
MTHFD1L	chr6:151302834-151303225	TRUE		intron		Up
MTM1	chrX:149416808-149417080			1st intron		Down
MTSS1	chr8:125821090-125821553	TRUE		5'	11534	Down
MTSS1	chr8:125857071-125858261	TRUE	TRUE	5'	47850	Down
MTSS1	chr8:125706708-125707476	TRUE		5'	57028	Down
MTX2	chr2:177028879-177029745			3'	1206	Up
MUC8	chr12:131591595-131591914			3'	62699	Down
MXI1	chr10:112022749-112023631	TRUE		intron		Up

MYC	chr8:128819877-128821548		TRUE	intron		Up
MYO1B	chr2:192206407-192207125			3'	91375	Up
MYO1C	chr17:1335300-1335950		TRUE	5'	1290	Down
MYO1G	chr7:44798312-44799588	TRUE	TRUE	5'	7364	Down
NAGK	chr2:71210155-71210816			intron		Down
NANS	chr9:97895116-97895701		TRUE	5'	3078	Up
NASP	chr1:45721943-45722677			1st intron		Up
NCL	chr2:232153943-232154292	TRUE	TRUE	1st intron		Up
NCOA2	chr8:71463891-71464253			1st intron		Down
NCOA3	chr20:45565977-45566329			1st intron		Down
NDUFB6	chr9:32562874-32563234			5'	0	Up
NEDD4L	chr18:53881623-53882846			1st intron		Down
NES	chr1:153465770-153466642			5'	5613	Down
NFATC1	chr18:75288046-75288399	TRUE		intron		Down
NFATC1	chr18:75321943-75322503	TRUE		intron		Down
NFKB2	chr10:104144125-104144920		TRUE	1st intron		Down
NIFIE14	chr19:40727695-40728973	TRUE	TRUE	intron		Up
NIN	chr14:50366657-50367240		TRUE	intron		Up
NME1	chr17:46585830-46586802	TRUE		1st intron		Up
NME4	chr16:385131-385860			5'	1879	Up
NMI	chr2:151979409-151980034			5'	7817	Down
NOL6	chr9:33464033-33464270			5'	302	Up
NOLA2	chr5:177512019-177512806			intron		Up
NOLC1	chr10:103919400-103921597	TRUE	TRUE	3'	7447	Up
NOP5/NOP58	chr2:202955904-202956468	TRUE	TRUE	1st intron		Up
NP	chr14:20007012-20007855			5'	62	Up
NPDC1	chr9:137216273-137216859		TRUE	5'	124	Up
NPHP4	chr1:5875249-5876218	TRUE		intron		Up
NPM1	chr5:170747835-170748452	TRUE		1st intron		Up
NPM3	chr10:103532545-103533366	TRUE		5'	36	Up
NR3C1	chr5:142763564-142764184		TRUE	5'	785	Down
NR4A1	chr12:50724771-50725584			1st intron		Down
NRD1	chr1:52054591-52055351		TRUE	1st intron		Down
NSEP1	chr1:42817774-42818173	TRUE	TRUE	1st intron		Up
NUMB	chr14:72994112-72994743		TRUE	1st intron		Down
NUMB	chr14:72989168-72989500			1st intron		Down
NUP153	chr6:17814032-17814719	TRUE	TRUE	5'	166	Up
NUP155	chr5:37406831-37407179			5'	35	Up
OAS1	chr12:111806811-111808244	TRUE		1st intron		Down
OLFML2A	chr9:124669709-124674333	TRUE	TRUE	3'	13221	Down
OPRS1	chr9:34626888-34628157	TRUE	TRUE	intron		Up
OPTN	chr10:13174035-13174496			5'	7833	Down
OSBPL10	chr3:31976816-31977413			1st intron		Down
OXTR	chr3:8791296-8791823			5'	5495	Down
P15RS	chr18:31901331-31901711			5'	47	Up
PA2G4	chr12:54785115-54785669	TRUE		1st intron		Up
PACS1	chr11:65694488-65695059			1st intron		Down
PAF53	chr9:37476971-37477765	TRUE		1st intron		Up
PAFAH1B3	chr19:47498206-47498901	TRUE		5'	95	Up
PAICS	chr4:57143317-57143689	TRUE		intron		Up
PAX5	chr9:37018801-37019498			1st intron		Down

PBEF1	chr7:105517326-105519422		TRUE	1st intron		Up
PCCB	chr3:137452339-137452816	TRUE		1st intron		Up
PCCB	chr3:137442735-137448493			5'	4471	Up
PCDH9	chr13:66604835-66605748			1st intron		Down
PCDH9	chr13:66702457-66702893	TRUE	TRUE	5'	2017	Down
PCSK7	chr11:116588916-116591666	TRUE		intron		Down
PDE7A	chr8:66862474-66862977			1st intron		Down
PDIFR	chr3:124268295-124269214	TRUE	TRUE	5'	0	Up
PEA15	chr1:156988452-156988963		TRUE	1st intron		Down
PELO	chr5:52131707-52132296			intron		Up
PFAAP5	chr13:32010884-32011192			5'	70	Down
PFDN2	chr1:157884564-157885533		TRUE	intron		Up
PFTK1	chr7:89894708-89895548	TRUE		5'	88252	Down
PGAM1	chr10:99175754-99176837		TRUE	5'	0	Up
PGAP1	chr2:197615823-197616304			1st intron		Up
PHF11	chr13:48967540-48968381		TRUE	5'	14	Down
PHF17	chr4:130089107-130089834	TRUE		1st intron		Up
PIGL	chr17:16070429-16070870			1st intron		Up
PIGL	chr17:16114730-16118432	TRUE		intron		Up
PIK3CD	chr1:9648041-9648820	TRUE		1st intron		Down
PIP5K3	chr2:209051261-209051671			3'	5864	Down
PLA2G12A	chr4:111013650-111014833	TRUE	TRUE	5'	4983	Up
PLCB2	chr15:38375127-38375615			intron		Down
PLEK	chr2:68508460-68508868			1st intron		Down
PLEK	chr2:68503628-68504185			5'	54	Down
PLEKHG2	chr8:96206729-96207177			5'	8191	Down
PNAS-4	chr1:241150311-241151595			1st intron		Up
PNOC	chr8:28223097-28223744			5'	7225	Down
PNPO	chr17:43373374-43374118	TRUE		5'	198	Up
POLR1B	chr2:113029725-113030524			intron		Up
POLR2I	chr19:41294296-41294960	TRUE	TRUE	3'	1786	Up
POLR3E	chr16:22216111-22217475	TRUE	TRUE	1st intron		Up
POLR3E	chr16:22221152-22221656			1st intron		Up
POLR3G	chr5:89806299-89806739	TRUE		1st intron		Up
POLR3G	chr5:89812853-89813452			1st intron		Up
POM121	chr7:71742764-71743884	TRUE	TRUE	5'	51215	Up
PP	chr10:71663119-71663590	TRUE		5'	79	Up
PPM1A	chr14:59891849-59892612	TRUE		3'	62306	Down
PPRC1	chr10:103883008-103883566	TRUE		1st intron		Up
PRCC	chr1:153550798-153551541		TRUE	1st intron		Up
PREX1	chr20:46825824-46827084	TRUE		1st intron		Down
PREX1	chr20:46871486-46872063			1st intron		Down
PREX1	chr20:46791655-46793230	TRUE		intron		Down
PREX1	chr20:46682566-46683512			intron		Down
PREX1	chr20:46684842-46685486			intron		Down
PRG1	chr10:70516553-70516904			5'	1142	Down
PRKCE	chr2:45789911-45790390		TRUE	5'	775	Down
PRKCE	chr2:46074719-46075395	TRUE		intron		Down
PRKD2	chr19:51912081-51912564			5'	851	Down
PRO1855	chr17:45829605-45830117	TRUE		5'	77	Up
PSARL	chr3:185085254-185085863	TRUE	TRUE	5'	63	Up

PSMB5	chr14:22560465-22562514	TRUE	TRUE	3'	2583	Up
PSMD12	chr17:62759670-62760373			3'	4405	Up
PSPH	chr7:56014390-56016051			5'	56960	Up
PSTPIP1	chr15:75093915-75094403		TRUE	1st intron		Down
PTD004	chr2:174938559-174939171	TRUE		5'	1715	Up
PTK2B	chr8:27243309-27244399		TRUE	1st intron		Down
PTMA	chr2:232397421-232397994	TRUE		5'	1137	Up
PTP4A1	chr6:64290642-64291568			1st intron		Up
PTPN9	chr15:73645138-73645564			1st intron		Down
PTPRC	chr1:195353198-195353639			1st intron		Down
PTPRG	chr3:61987263-61990077	TRUE		intron		Down
PWP1	chr12:106574205-106574994		TRUE	5'	7179	Up
QTRT1	chr19:10673058-10673547	TRUE	TRUE	5'	0	Up
RABGGTB	chr1:75963736-75964194		TRUE	1st intron		Up
RAC3	chr17:77583397-77583625	TRUE		1st intron		Up
RAD23A	chr19:12917233-12917634	TRUE	TRUE	5'	177	Up
RAD51L1	chr14:68164333-68166305		TRUE	3'	32119	Down
RAD51L1	chr14:68042823-68043521	TRUE		intron		Down
RAD54L	chr1:46424644-46425163	TRUE		5'	1070	Up
RAFTLIN	chr3:16478305-16479036			intron		Down
RAFTLIN	chr3:16385530-16385953	TRUE		intron		Down
RALA	chr7:39545794-39546639	TRUE		3'	25130	Up
RALB	chr2:120724245-120725124			5'	1983	Down
RALGPS1	chr9:127069928-127070226			3'	5031	Down
RALGPS1	chr9:127008485-127009257	TRUE		intron		Down
RALGPS1	chr9:127056742-127058042	TRUE		intron		Down
RANGAP1	chr22:40005920-40007050		TRUE	5'	3083	Up
RAP1GDS1	chr4:99573780-99574409			1st intron		Up
RAPGEF1	chr9:131620930-131623539		TRUE	5'	6814	Down
RARS	chr5:167892008-167892168			3'	13175	Up
RASGRP2	chr11:64264562-64264991			intron		Down
RASSF2	chr20:4743530-4744131	TRUE		intron		Down
RBM14	chr11:66140582-66141532		TRUE	5'	0	Up
RBMS3	chr3:29384744-29385298			1st intron		Down
RBMS3	chr3:29391283-29391755			1st intron		Down
RBMX	chrX:135683521-135689383			1st intron		Up
RECK	chr9:36038331-36038628			1st intron		Down
RFT1	chr3:53139183-53139520			1st intron		Up
RGS1	chr1:189271741-189272360			5'	4454	Down
RGS19	chr20:62180633-62181656	TRUE		5'	291	Down
RIPX	chr4:71935859-71936658	TRUE	TRUE	1st intron		Down
RNPC2	chr20:33793360-33794031		TRUE	5'	63	Down
ROR1	chr1:63998659-63999165			1st intron		Down
ROR1	chr1:64023945-64024256			1st intron		Down
RPS6KA5	chr14:90556856-90557455			1st intron		Down
RUVBL1	chr3:129278047-129278335			3'	4410	Up
SAE1	chr19:52405631-52405986	TRUE		3'	566	Up
SAP30	chr4:174665640-174666257		TRUE	5'	710	Up
SCAP	chr3:47492403-47492662	TRUE	TRUE	5'	39	Up
SCO2	chr22:49253319-49253912			1st intron		Up
SDCCAG3	chr9:136580234-136581058	TRUE	TRUE	5'	92	Up

SDF2L1	chr22:20321300-20322211		TRUE	intron		Up
SDHA	chr5:272310-272743			1st intron		Up
SEC14L1	chr17:72755598-72759362	TRUE	TRUE	3'	31208	Down
SEC14L1	chr17:72647781-72648693		TRUE	5'	111	Down
SEC61A2	chr10:12205429-12211219			5'	2333	Down
SEMA4D	chr9:89282257-89282965			intron		Down
SEMA6A	chr5:115807615-115808560	TRUE		3'	0	Down
SEMA6A	chr5:115938637-115938931			5'	734	Down
SEPHS1	chr10:13425272-13426905			1st intron		Up
SERPINF1	chr17:1614316-1614758	TRUE		1st intron		Up
SESTD1	chr2:179808210-179808812			1st intron		Down
SESTD1	chr2:179723997-179724874	TRUE		3'	75355	Down
SETBP1	chr18:40783837-40784296	TRUE		intron		Down
SF1	chr11:64301625-64302346		TRUE	1st intron		Down
SFPQ	chr1:35327380-35327952			5'	0	Up
SFRS10	chr3:187137967-187139041		TRUE	5'	0	Up
SFXN4	chr10:120914869-120915292	TRUE	TRUE	5'	0	Up
SGPP2	chr2:223155887-223156244			1st intron		Down
SHFM3	chr10:103444581-103445105	TRUE	TRUE	5'	0	Down
SHMT1	chr17:18214236-18215001			5'	7282	Up
SIAT9	chr2:86038381-86039231			5'	11174	Down
SKIL	chr3:171558126-171559418		TRUE	5'	1844	Down
SLA	chr8:134139996-134140592			1st intron		Down
SLC11A2	chr12:49705797-49706538		TRUE	1st intron		Up
SLC16A1	chr1:113212149-113212465			5'	1470	Up
SLC16A6	chr17:63798955-63799611	TRUE	TRUE	5'	356	Down
SLC19A1	chr21:45885398-45886880		TRUE	5'	99184	Up
SLC25A13	chr7:95595413-95596373	TRUE	TRUE	5'	0	Up
SLC27A4	chr9:128182393-128183014		TRUE	5'	0	Up
SLC2A4RG	chr20:61842752-61843190	TRUE		intron		Up
SLC2A5	chr1:9061353-9061949	TRUE		1st intron		Down
SLC30A5	chr5:68328248-68328774			5'	97154	Up
SLC35F2	chr11:107284917-107285737			1st intron		Up
SLC39A3	chr19:2694321-2694891			5'	3478	Up
SLC39A8	chr4:103619958-103620490			1st intron		Up
SLC3A2	chr11:62373256-62373653			5'	6761	Up
SLC7A5	chr16:86397700-86397989	TRUE		3'	23339	Up
SLU7	chr5:159773494-159774083			intron		Down
SMC2L1	chr9:103969195-103970241	TRUE		intron		Up
SMYD2	chr1:210843215-210843714	TRUE		1st intron		Up
SNRPB2	chr20:16612695-16613644			5'	45416	Up
SNRPD1	chr18:17446854-17451766			1st intron		Up
SNX5	chr20:17896866-17897497	TRUE	TRUE	5'	89	Up
SNX9	chr6:158188533-158192944	TRUE		1st intron		Down
SOCS1	chr16:11256060-11256440		TRUE	3'	0	Down
SOCS3	chr17:73867376-73867859			5'	0	Down
SORD	chr15:43103058-43103552	TRUE		1st intron		Up
SORL1	chr11:121102098-121104407	TRUE		3'	97509	Down
SOX12	chr20:252518-253621	TRUE	TRUE	5'	1331	Up
SPATA13	chr13:23643264-23643493			1st intron		Up
SPRED2	chr2:65454911-65455372			intron		Down

SRP72	chr4:57174516-57175257	TRUE		1st intron		Up
SRPRB	chr3:135006764-135007357			5'	228	Up
SSBP3	chr1:54640352-54641437			5'	56949	Down
SSR3	chr3:157784015-157787803	TRUE		5'	29355	Up
ST7	chr7:116288835-116289497			1st intron		Up
STARD10	chr11:72182408-72182762	TRUE		5'	276	Down
STAT3	chr17:37794256-37794642	TRUE	TRUE	5'	390	Down
STRAD13	chr17:77573069-77573859		TRUE	1st intron		Up
STRBP	chr9:123035239-123035781			1st intron		Down
SUCLG2	chr3:67778196-67779260			1st intron		Up
SWAP70	chr11:9644294-9645520	TRUE		1st intron		Down
SYK	chr9:90681065-90681456			1st intron		Down
SYNCVIP	chr6:86445330-86445547		TRUE	5'	36130	Up
SYNGR3	chr16:1982483-1983297		TRUE	intron		Up
TA-NFKBH	chr19:41078053-41078737			intron		Down
TBC1D4	chr13:74952804-74953543	TRUE	TRUE	1st intron		Up
TBC1D4	chr13:74958300-74958892			5'	4203	Up
TBC1D5	chr3:17235678-17236271			intron		Down
TBC1D5	chr3:17759682-17760338	TRUE		5'	2464	Down
TBC1D5	chr3:17343876-17347244	TRUE		intron		Down
TBCE	chr1:231855575-231856754	TRUE	TRUE	5'	688	Up
TCIRG1	chr11:67561928-67563496			5'	857	Down
TFEB	chr6:41783220-41783946	TRUE	TRUE	intron		Down
TFEB	chr6:41804668-41805505			intron		Down
TGOLN2	chr2:85466547-85466952		TRUE	5'	0	Down
THRAP2	chr12:115275472-115280556	TRUE	TRUE	5'	98774	Down
TIM14	chr3:182191335-182191843			5'	1422	Up
TIP120A	chr12:65979512-65979905			1st intron		Up
TKT	chr3:53263791-53264903	TRUE	TRUE	1st intron		Up
TLE3	chr15:68175161-68175705			intron		Down
TLR4	chr9:117545848-117546522			5'	30	Down
TLR4	chr9:117621191-117621960	TRUE		3'	62546	Down
TMEPAI	chr20:55749774-55750908	TRUE		5'	31301	Down
TMEPAI	chr20:55799086-55801244	TRUE	TRUE	5'	81174	Down
TOMM20	chr1:231593449-231593903		TRUE	3'	5031	Up
TOMM70A	chr3:101601866-101602899		TRUE	5'	0	Up
TRAF1	chr9:120766939-120768627			intron		Down
TRIM2	chr4:154587064-154587575			1st intron		Down
TRIM8	chr10:104395938-104396667			1st intron		Down
TRIM8	chr10:104394011-104395105	TRUE	TRUE	5'	0	Down
TRIP13	chr5:976045-976469			3'	5148	Up
TRNT1	chr3:3143741-3144321	TRUE	TRUE	1st intron		Up
TSAP6	chr2:119694706-119695920			5'	2705	Up
TSN	chr2:122228793-122229471	TRUE	TRUE	5'	259	Up
TTC17	chr11:43337076-43337664		TRUE	1st intron		Down
TTC17	chr11:43330129-43331227			5'	6105	Down
TTC3	chr21:37470231-37470921	TRUE		intron		Up
TTC9	chr14:70195704-70196481			1st intron		Down
TTF2	chr1:117313954-117314407			5'	824	Up
TXNDC	chr14:50782625-50783033	TRUE		intron		Up
TXNL2	chr10:131799565-131800336			5'	24882	Up

TXNRD1	chr12:103184002-103184237			1st intron		Up
TXNRD1	chr12:103182917-103183547	TRUE		5'	0	Up
U2AF1	chr21:43377396-43380263	TRUE		3'	7285	Up
UBE2C	chr20:43874180-43874515	TRUE		5'	387	Up
UBE2D3	chr4:104062778-104063778	TRUE		3'	10997	Down
UBQLN1	chr9:83552343-83553175		TRUE	5'	102	Up
UCP2	chr11:73371930-73372329	TRUE	TRUE	5'	598	Down
UGCG	chr9:111801907-111802917	TRUE		3'	27438	Down
USP14	chr18:96509-101573			5'	50229	Up
UTRN	chr6:144663192-144663556			1st intron		Down
UTX	chrX:44527899-44528673			1st intron		Down
VAV2	chr9:133648555-133649908	TRUE		3'	7199	Down
VAV2	chr9:133718171-133720275	TRUE		intron		Down
VDAC1	chr5:133368148-133368908		TRUE	5'	186	Up
WARS2	chr1:119252161-119252914			3'	34594	Up
WASPIP	chr2:175283953-175284228			1st intron		Down
WASPIP	chr2:175314985-175315486			1st intron		Down
WDFY2	chr13:51097374-51098247			1st intron		Down
WDR18	chr19:935143-935685		TRUE	5'	0	Up
WDR37	chr10:1081433-1085828		TRUE	5'	1092	Down
WDR37	chr10:1159078-1159494	TRUE		intron		Down
WDR4	chr21:43171827-43172316	TRUE	TRUE	1st intron		Up
WDR4	chr21:43172481-43172879			5'	0	Up
WRB	chr21:39672449-39678307	TRUE	TRUE	1st intron		Up
XPO4	chr13:20374014-20374538	TRUE		1st intron		Up
XPO5	chr6:43650905-43651496	TRUE		1st intron		Up
XPO6	chr16:28130732-28131168			5'	700	Up
ZBTB4	chr17:7322926-7323797		TRUE	1st intron		Down
ZBTB4	chr17:7314248-7314836			1st intron		Down
ZC3HDC1	chr7:139215506-139215792		TRUE	5'	0	Down
ZCCHC7	chr9:37068841-37069778	TRUE		5'	40922	Down
ZDHHC11	chr5:825485-826980	TRUE		3'	22614	Up
ZFHXB1	chr2:144980485-144981188	TRUE	TRUE	3'	0	Down
ZFP36	chr19:44591865-44592372			3'	303	Down
ZFYVE1	chr14:72563398-72563911		TRUE	5'	110	Down
ZFYVE1	chr14:72567446-72571903		TRUE	5'	7862	Down
ZHX1	chr8:124327323-124332624	TRUE		intron		Up
ZNF224	chr19:49305888-49306117			3'	1701	Down
ZNF224	chr19:49306169-49306514			3'	1979	Down
ZNF274	chr19:63383616-63388232		TRUE	5'	2561	Down
ZNF302	chr19:39916820-39917587		TRUE	intron		Down
ZNF598	chr16:1996997-1997459	TRUE		1st intron		Up
ZNF598	chr16:1998842-1999506		TRUE	1st intron		Up
ZNF614	chr19:57222973-57223587			1st intron		Up
ZNF74	chr22:19075138-19075341			intron		Up
ZNFN1A1	chr7:50212554-50213110			5'	5642	Down
ZZZ3	chr1:77859876-77861148	TRUE	TRUE	1st intron		Up

Supplemental Table ST6: Potential Myc targeted miRNAs

PET Cluster ID	Cluster Binding Location	Binding location	miRNA Target	Previous Expression evidence
7.25763471	chr7:25763471-25764373	5' (625)	mir-148a	human hepatocyte
9.94007676	chr9:94007676-94008076	5' (9717)	let-7a-1	HuES cells
9.94015722	chr9:94015722-94016098	5' (1695)	let-7a-1	HuES cells
10.88008518	chr10:88008518-88008967	3' (5457)	mir-346	computational prediction
13.90799144	chr13:90799144-90799791	5' (1068)	mir-17	HeLa cells
17.4406286	chr17:44062860-44063470	3' (1381)	mir-196	human osteoblast sarcoma cells
20.61282553	chr20:61282553-61283465	3' (2170)	mir-124	HuES cells
21.25861042	chr21:25861042-25861339	5' (6824)	mir-155	human HL-60 leukemia cells

Supplemental Table ST8: Functional annotation of Myc direct targets

668 Myc direct targets	# of genes	P value
Biological Process		
Nucleoside, nucleotide and nucleic acid metabolism	140	2.02E-07
Protein metabolism and modification	119	2.50E-04
mRNA splicing	19	6.59E-04
Cell cycle	45	3.75E-03
Pre-mRNA processing	21	4.93E-03
Protein modification	55	6.19E-03
Embryogenesis	13	1.70E-02
Intracellular signaling cascade	43	1.72E-02
Purine metabolism	9	1.93E-02
rRNA metabolism	9	2.68E-02
tRNA metabolism	7	3.25E-02
Oncogenesis	25	3.68E-02
Cell cycle control	24	4.05E-02
Molecular Functions		
Synthase and synthetase	24	1.23E-06
Nucleic acid binding	110	7.12E-05
Select regulatory molecule	59	2.68E-04
Synthetase	12	8.50E-04
Guanyl-nucleotide exchange factor	15	2.18E-03
G-protein modulator	27	3.54E-03
Chaperone	16	4.29E-03
Other ligase	14	1.83E-02
Ligase	24	2.85E-02
Other RNA-binding protein	14	2.91E-02
Other chaperones	11	3.61E-02
Pathways		
B cell activation	14	1.41E-04
Inflammation mediated by chemokine and cytokine	23	4.59E-03
T cell activation	13	5.27E-03
De novo purine biosynthesis	7	7.89E-03
49 transcription factors directly regulated by Myc	GENE Symbol	Expression
basic helix-loop-helix domain containing, class B, 3	BHLHB3	Down
core-binding factor, runt domain, alpha subunit 2	CBFA2T2	Down

core-binding factor, runt domain, alpha subunit 2	CBFA2T3	Down
CCAAT/enhancer binding protein (C/EBP), beta	CEBPB	Up
core promoter element binding protein	COPEB	Down
cold shock domain protein A	CSDA	Up
estrogen receptor 2 (ER beta)	ESR2	Down
ets variant gene 6 (TEL oncogene)	ETV6	Down
FLJ25476 protein	FLJ25476	Down
forkhead box P4	FOXP4	Down
hypermethylated in cancer 2	HIC2	Up
interferon regulatory factor 2	IRF2	Down
interferon regulatory factor 5	IRF5	Down
v-jun sarcoma virus 17 oncogene homolog (avian)	JUN	Down
MAX interactor 1	MAX	Up
MYC-associated zinc finger protein	MAZ	Up
myeloid/lymphoid or mixed-lineage leukemia	MLLT3	Down
male-specific lethal 3-like 1 (Drosophila)	MSL3L1	Down
MAX interactor 1	MXI1	Up
v-myc myelocytomatosis viral oncogene homolog (avian)	MYC	Up
nuclear receptor coactivator 2	NCOA2	Down
nuclear factor of activated T-cells	NFATC1	Down
nuclear factor of kappa light polypeptide gene enhancer	NFKB2	Down
nucleoside phosphorylase	NP	Up
nuclear receptor subfamily 4, group A, member 1	NR4A1	Down
nuclease sensitive element binding protein 1	NSEP1	Up
paired box gene 5 (B-cell lineage specific activator protein)	PAX5	Down
PHD finger protein 17	PHF17	Up
peroxisome proliferative activated receptor, gamma	PPRC1	Up
nuclear phosphoprotein similar to S. cerevisiae PWP1	PWP1	Up
ras-related C3 botulinum toxin substrate 3	RAC3	Up
receptor tyrosine kinase-like orphan receptor 1	ROR1	Down
RuvB-like 1 (E. coli)	RUVBL1	Up
splicing factor 1	SF1	Down
SKI-like	SKIL	Down
SET and MYND domain containing 2	SMYD2	Up
SRY (sex determining region Y)-box 12	SOX12	Up
signal transducer and activator of transcription 3	STAT3	Down
stimulated by retinoic acid 13	STRA13	Up
transcription factor EB	TFEB	Down
TBP-interacting protein	TIP120A	Up
transducin-like enhancer of split 3	TLE3	Down
transcription termination factor, RNA polymerase II	TTF2	Up
zinc fingers and homeoboxes 1	ZHX1	Up
zinc finger protein 224	ZNF224	Down
zinc finger protein 274	ZNF274	Down
zinc finger protein 302	ZNF302	Down
zinc finger protein 614	ZNF614	Up
zinc finger protein 74 (Cos52)	ZNF74	Up

III. Detailed materials and methods

Cell culture and chromatin immunoprecipitation

P493-6 cells were the generous gift of Dr. Eick at the Institute for Clinical Molecular Biology and Tumor Genetics, GSF-Research Centre, Munich, Germany. Cells were cultured in RPMI 1640, 10% fetal calf serum, and penicillin-streptomycin (Pen-Strep) in a 5% CO₂ humidified incubator. To repress *MYC* transgene expression, cells were treated with RPMI 1640-10% fetal calf serum-Pen-Strep supplemented with 0.1 µg/ml tetracycline (Sigma) for 72 hr. Approximately 10⁹ P493-6 cells were crosslinked with formaldehyde, and chromatin was immunoprecipitated as previously described (8). Rabbit polyclonal c-Myc (sc-764), Santa Cruz Biotechnology), E2F1 (sc-193, Santa Cruz) and HGF antibodies (sc-7949), Santa Cruz) were used at a ratio of 1ug antibody: chromatin from 2X10⁷ cells, to immunoprecipitate chromatin fragments.

ChIP-PET experiment

Using the Myc ChIP enriched DNA fragments, a Myc ChIP-PET library was constructed as previously described (Wei et al 2006). Briefly, the ChIP enriched DNA were cloned into the cloning vector pGIS3 to generate the ChIP DNA library. Purified plasmid from the ChIP DNA library was digested with MmeI to release the internal fragments and a signature tag from each terminal of the original ChIP DNA insert were self-ligated to form a “single-ditag library”. 50 bp paired end ditags (PETs) were released by BamHI, PAGE-purified and concatenated to clone into pZErO-1 to form the final ChIP-PET library for sequencing. PET sequences were extracted from the raw reads and mapped to human genome sequence assembly (hg17). The process of PET extraction and mapping is essentially same as previously described for cDNA analysis (9). The mapping criteria are

that both the 5' and 3' signatures must have minimal 17 bp match, present on the same chromosome and same strand, in the correct orientation (5'→3'), and within 6kb of genomic distance.

Quantitative PCR assay

Quantitative PCR analyses were performed using ABI PRISM 7900 sequence Detection System and SYBR Green master mix as previously described (10). Relative occupancy values were calculated by determining the apparent immunoprecipitation efficiency (ratios of the amount of immunoprecipitated DNA over that of the input sample) and normalized to the level observed at a control region, which was defined as 1.0. The error for independent determinations is ±10%. Primers for validation of ChIP-PET loci are available in the supplemental table ST3.

Gene expression profiling analysis using microarray

Total RNA isolated from both p493 cells and cells treated with tetracycline were used to probe Affymetrix U133 plus 2.0 array following manufacturer's recommendation. Fluorescence was detected using the GeneChip Scanner and resulting images were analyzed by software provided by Affymetrix. The initial analysis was based on pairwise comparison between samples treated from two experiment conditions. To select differentially expressed genes, we used SAM (Significance Analysis of Microarrays). In SAM, the relative difference ($d(i)$) is compared to the distribution of $d(i)$ following random permutation of the sample categories. For each $d(i)$, a certain proportion of all genes in the permutation set (control set) will be found to be 'significant' by chance and this parameter is then used to calculate a "False Discovery Rate" (FDR). Among 688 Affymetrix probesets, the ratio of signal intensity values was ranged between 1.8 and

12.1 for MYC up regulated genes and between 1.6 and 10.9 for MYC down-regulated genes.

V. References:

1. Kuznetsov, V. A. (2005) in *ISAGE: Current Technologies and Applications*, ed. Wang, S. M. (Horizon BioScience, Norwich, United Kingdom), pp. 139–180.
2. Wei, C. L., Wu, Q., Vega, V. B., Chiu, K. P., Ng, P., Zhang, T., Shahab, A., Yong, H. C., Fu, Y., Weng, Z., Liu, J., Zhao, X. D., Chew, J. L., Lee, Y. L., Kuznetsov, V. A., Sung, W. K., Miller, L. D., Lim, B., Liu, E. T., Yu, Q., Ng, H. H. & Ruan, Y. (2006) *Cell* **124**, 207-19.
3. Pavese, G., Mauri, G. & Pesole, G. (2001) *Bioinformatics* **17 Suppl 1**, S207-14.
4. Hosack, D. A., Dennis, G., Jr., Sherman, B. T., Lane, H. C. & Lempicki, R. A. (2003) *Genome Biol* **4**, R70.
5. Li, Z., Van Calcar, S., Qu, C., Cavenee, W. K., Zhang, M. Q. & Ren, B. (2003) *Proc Natl Acad Sci U S A* **100**, 8164-9.
6. Fernandez, P. C., Frank, S. R., Wang, L., Schroeder, M., Liu, S., Greene, J., Cocito, A. & Amati, B. (2003) *Genes Dev* **17**, 1115-29.
7. Cawley, S., Bekiranov, S., Ng, H. H., Kapranov, P., Sekinger, E. A., Kampa, D., Piccolboni, A., Sementchenko, V., Cheng, J., Williams, A. J., Wheeler, R., Wong, B., Drenkow, J., Yamanaka, M., Patel, S., Brubaker, S., Tammana, H., Helt, G., Struhl, K. & Gingeras, T. R. (2004) *Cell* **116**, 499-509.
8. Boyd, K. E. & Farnham, P. J. (1997) *Mol Cell Biol* **17**, 2529-37.
9. Ng, P., Wei, C. L., Sung, W. K., Chiu, K. P., Lipovich, L., Ang, C. C., Gupta, S., Shahab, A., Ridwan, A., Wong, C. H., Liu, E. T. & Ruan, Y. (2005) *Nat Methods* **2**, 105-11.
10. Loh, Y. H., Wu, Q., Chew, J. L., Vega, V. B., Zhang, W., Chen, X., Bourque, G., George, J., Leong, B., Liu, J., Wong, K. Y., Sung, K. W., Lee, C. W., Zhao, X. D., Chiu, K. P., Lipovich, L., Kuznetsov, V. A., Robson, P., Stanton, L. W., Wei, C. L., Ruan, Y., Lim, B. & Ng, H. H. (2006) *Nat Genet* **38**, 431-40.